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        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

GGCAGAGCCT CAAGCTGACT TGGATTATGT GGTCCCTCAA ATCTACCGAC ACATGCAGGA   60

GGAGTTCCGG GGCCGGTTAG AGAGGACCAA ATCTCAGGGT CCCCTGACTG TGGCTGCTTA   120

TCAKWYGGGG AGTGTCTACT CAGCTGCTAT GGTCACAGCC CTCACCCTGT TGGCCTTCCC   180

ACTTCTGCTG TTGCATGCGG AGCGCATCAG CCTTGTGTTC CTGCTTCTGT TTCTGCAGAG   240

CTTCCTTCTC CTACATCTGC TTGCTGCTGG GATACCCGTC ACCACCCCTG GTCCTTTTAC   300

TGTGCCATGG CAGGCAGTCT CGGCTTGGGC CCTCATGGCC ACACAGACCT TCTACTCCAC   360

AGGCCACCAG CCTGTCTTTC CAGCCATCCA TTGGCATGCA GCCTTCGTGG GATTCCCAGA   420

GGGTCATGGC TCCTGTACTT GGCTGCCTGC TTTGCTAGTG GGAGCCAACA CCTTTGCCTC   480

CCACCTCCTC TTTGCAGTAG GTTGCCCACT GCTCCTGCTC TGGCCTTTCC TGTGTGAGAG   540

TCAAGGGCTG CGGAAGAGAC AGCAGCCCCC AGGGAATGAA GCTGATGCCA GAGTCAGACC   600

CGAGGAGGAA GAGGAGCCAC TGATGGAGAT GCGGCTCCGG GATGCGCCTC AGCACTTCTA   660

TGCAGCACTG CTGCAGCTGG GCCTCAAGTA CCTCTTTATC CTTGGTATTC AGATTCTGGC   720

CTGTGCCTTG GCAGCCTCCA TCCTTCGCAG GCATCTCATG GTCTGGAAAG TGTTTGCCCC   780

TAAGTTCATA TTTGAGGCTG TGGGCTTCAT TGTGAGCAGC GTGGGACTTC TCCTGGGCAT   840

AGCTTTGGTG ATGAGAGTGG ATGGTGCTGT GAGCTCCTGG TTCAGGCAGC TATTTCTGGC   900

CCAGCAGAGG TAGCCTAGTC TGTGATTACT GGCACTTGGC TACAGAGAGT GCTGGAGAAC   960

AGTGTAGCCT GGCCTGTACA GGTACTGGAT GATCTGCAAG ACAGGCTCAG CCATACTCTT   1020

ACTATCATGC AGCCAGGGGC CGCTGACATC TANGACTTCA TTATTCWATR ATTCAGGACC   1080

ACAGTGGAGT ATGATCCCTA ACTCCTGATT TGGATGCATC TGAGGGACAA GGGGGKCGGT   1140

STCCGAAGTG GAATAAAATA GGCGGGCGTG GTGACTTGCA CCT   1183

    (2) INFORMATION FOR SEQ ID NO: 148:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 734 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

GAATTCGGCA GAGTGAAGCA TTAGAATGAT TCCAACACTG CTCTTCTGCA CCATGAGACC   60

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AACCCAGGGC AAGATCCCAT CCCATCACAT CAGCCTACCT CCCTCCTGGC TGCTGGCCAK    120

GATGTCGCCA GCATTACCTT CCACTGCCTT TCTCCCTGGG AAGCAGCACA GCTGAGACTG    180

GGCACCAGGC CACCTCTGTT GGGACCCACA GGAAAGAGTG TGGCAGCAAC TGCMTGGCTG    240

ACCTTTCTAT CTTCTCTAGG CTCAGGTACT GCTCCTCCAT GCCCATGGYT GGGCCGTGGG    300

GAGAAGAAGC TCTCATACGC CTTCCCACTC CCTCTGGTTT ATAGGACTTC ACTCCCTAGC    360

CAACAGGAGA GGAGGCCTCC TGGGGTTTCC CCRRGGCAGT AGGTCAAACG ACCTCATCAC    420

AGTCTTCCTT CCTCTTCAAG CGTTTCATGT TGAACACAGC TCTCTCCRCT CCCTTGTGAT    480

TTCTGAGGGT CACCACTGCC ARCCTCAGGC AACATAGAGA GCCTCCTGTT CTTTCTATGC    540

TTGGTCTGAC TGAGCCTAAA GTTGAGAAAA TGGGTGCCAA GGCCAGTGCC AGTGTCTTGG    600

GGCCCCTTTG GCTCTCCCTC ACTCTCTGAG GCTCCAGCTG GTCCTGGGAC ATGCAGCCAG    660

GACTGTGAGT CTGGGCASGT CCAAGGCCTG CACCTTCAAG AAGTGGAATA AATGTGGCCT    720

TTGCTTCTAT TTAA                                                      734
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(2) INFORMATION FOR SEQ ID NO: 149:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1405 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

```
GGCACAGTGG ACCCCAGACT CCCTCTCCGC CTTTCTCTGC CTGGGGAGAC CCACTGTGTG    60

CATGGCATCA CTGACTCCCA TACCTCTGGC TATCAAAGGT TTCTGCCATG GCCACCCTGG    120

AAGSAAACCA GAGGGAGGTA GACAGGGAGA TCAGGTCCCT TCTACTCTGG TTCCTGCTCT    180

GTGAAATTGT CTCAGGCTGG CTGTGTCCAG ARGGTCCCTG GTTCTCTCAR GGATGCCAAA    240

TCTACAAGAA TCTCTCCTCT TCCAGTTCCT ATAACCTCTC CTTCCTTTTG TCTCTTTAGA    300

CCTTGGAGTA GTAGCAGCCA GGTTCTTTCT ATCTCTGGGT TAGTGCATTA TCTCTGGTGG    360

CTCCCTTACC CAGGACTTTG GGAATGGTCT TTTTGTAATA CATTCTCCTC AAATAATTCA    420

ATTTTGAGTG TTCTGTATGT ATCCTGCTGG GAGGTTGTTA TATACAAATC ACTGTGCCCG    480

TTTAGCAGAG AAGGAGACTG AAGCTCAGGG AGGTTAAGTG TCTTTCTCTA GGTCGTATTG    540

TGGAGAAAGT GGCTGACTGG GGACTTGAAT GAGGTCCCTA GTTTCATGCT CGGAGGGCAA    600

AGANGAATGT CCAATTGGCC TGAGATAAGC CTCTGGTAAA ATGTACTGTA CATAATAGGT    660

AATCAATAAA TGTTGGCTGA TGACAAACAT GTTTTCTTTG TTCATTAGTT ATAGTGATTA    720
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     TGTTCTAAAT AACTCCMACA AGGAARTCAG CACATTTGGA ATATCAWTAT CTTTCCATGA     780

     TAATATCTTT CCMYGGAAAG AWAATGATAT TCCMAACTGG GAGTGTCCCW AGCARATCTG     840
5
     ANTCTGTGTA TTGGCCCTGG GGTGGGCCAG CCCCTTAGAC TCTATGGTCT CATTCTCTTT     900

     GTTTACAAAA TTGAGATAAG GCCTTATTCT CTCCCCACCC CACCCATCCA TATTGTTTTG     960
10
     AGAATAAAAT GAGAGGATGT GTGTCAAGGG TGTATTTTGG CAATAGTCTC TGAGCCATTT    1020

     TCTGAGCACC TCCATACTGT TGACACTCAA GTAATATTTC ATCAGCATTC CATTCAGGNT    1080
15
     CCTCCCTTAA TGAGGTGTGC GATGTACAAG AGTYGTGAGG TGGCAAAGGA TGGGCTCCTG    1140

     AGGAAACACT TAGGAAACTG GGCTTTCTGC CATTAAAAGA GACAAACCTT TGTGGTGACC    1200

     TAATTAAAGT TTTTAAAATT CAATTTGGAA AGTTAGCAAG CTAGCTCCTK TCCAGGWAAA    1260
20
     ATAAGGAGTC AGTGCATGAC CTAACCGGTC CCGGGCTGCT TGCCATTCCA AACAACTGCA    1320

     GTAAGTTTAT CACNTTCTTT CAGGGACTGA GGTTTCCAGG CACAGACTTG GATAAGGAAG    1380

     GATGTCCTAT GGGGTCACAT TGATG                                         1405
25


     (2) INFORMATION FOR SEQ ID NO: 150:
30
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 2890 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
35             (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

     TTATATGCTA CAGCTACAGT AATTTCTTCT CCAAGCACAG AGGANCTTTC CCAGGATCAG      60
40
     GGGGATCGCG CGTCACTTGA TGCTGCTGAC AGTGGTCGTG GGAGCTGGAC GTCATGCTCA     120

     AGTGGCTCCC ATGATAATAT ACAGACGATC CAGCACCAGA GAAGCTGGGA GACTCTTCCA     180

     TTCGGGCATA CTCACTTTGA TTATTCAGGG GATCCTGCAG GTTTATGGGC ATCAAGCAGC     240
45
     CATATGGACC AAATTATGTT TTCTGATCAT AGCACAAAGT ATAACAGGCA AAATCAAAGT     300

     AGAGAGAGCC TTGAACAAGC CCAGTCCCGA GCAAGCTGGG CGTCTTCCAC AGGTTACTGG     360
50
     GGAGAAGACT CAGAAGGTGA CACAGGCACA ATAAAGCGGA GGGGTGGAAA GGATGTTTCC     420

     ATTGAAGCCG AAAGCAGTAG CCTAACGTCT GTGACTACGG AAGAAACCAA GCCTGTCCCC     480
55
     ATGCCTGCCC ACATAGCTGT GGCATCAAGT ACTACAAAGG GGCTCATTGC ACGAAAGGAG     540

     GGCAGGTATC GAGAGCCCCC GCCCACCCCT CCCGGCTACA TTGGAATTCC CATTACTGAC     600

     TTTCCAGAAG GGCACTCCCA TCCAGCCAGG AAACCGCCGG ACTACAACGT GGCCCTTCAG     660
60
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AGATCGCGGA TGGTCGCACG ATCCTCCGAC ACAGCTGGGC CTTCATCCGT ACAGCAGCCA    720

CATGGGCATC CCACCAGCAG CAGGCCTGTG AACAAACCTC AGTGGCATAA AYCGAACGAG    780

TCTGACCCGC GCCTCGCCCC YTATCAGTCC CAAGGGTTTT CCACCGAGGA GGATGAAGAT    840

GAACAAGTTT CTGCTGTTTG AGGCACAGAC TTTTCTGGAA GCAGAGCGAG CCACCTGAAA    900

GGAGAGCACA AGAAGACGTC CTGAGCATTG GAGCCTTGGA ACTCACATTC TGAGGACGGT    960

GGACCAGTTT GCCTCCTTCC CTGCCTTAAA AGCAGCATGG GGSTTCTTCT CCCCTTCTTC    1020

CTTTCCCCTT TGCATGTGAA ATACTGTGAA GAAATTGCCC TGGCACTTTT CAGACTTTGT    1080

TGCTTGAAAT GCACAGTGCA GCAATCTTCG AGCTCCCACT GTTGCTGCCT GCCACATCAC    1140

ACAGTATCAT TCCAAATTCC AAGATCATCA CAACAAGATG ATTCACTCTG CTGCACTTC     1200

TCAATGCCTG GAAGGATTTT TTTTAATCTT CCTTTTAGAT TTCAATCCAG TCCTAGCACT    1260

TGATCTCATT GGGATAATGA GAAAAGCTAG CCATTGAACT ACTTGGGGCC TTTAACCCAC    1320

CAAGGAAGAC AAAGAAAAAC AATGAAATCC TTTGAGTACA GTGCTTGTCC ACTTGTTTAC    1380

AATGTCCTCC TTTTAAAAAA AAAAAAATGA GTTTAAAGAT TTTGTTCAGA GAGTAAATAT    1440

ATATCCATTT AATGATTACA GTATTATTTT AAACCTTAAG TAGGGTTGCC AGCCTGGTTT    1500

CTGAAAAACC AAAATATGCCG GACAGGGTGT GGCCACACCA AGAAGACGGG AAGACCTGGC    1560

TTGTGACCCT GGCTTCCCAT GTCCTTCTGG TCTCACCCGC GAAGTGCCCT ATCCTGGAAG    1620

TATGAAATGT TAGCCAATTA ATACCAAGAC ACCTCATCTG CTCCTTCCCC AGTGGATGGG    1680

GTTCTTCTGT AAAACTGTTT GCACATGGCC AGGGGAGGGA ACTAGGACCC TTGTGTCCTG    1740

TCTGAGCCTT ATGGAGGCAG GACGGTGTCA TTGGCGGATG TGTCCTGCTC CATTGAGATG    1800

GATGGCAAAC CCCATTTTTA AGTTATATTT CTTTGATTTT TGTTAATTTA GAGGTGTAGG    1860

TTTTGTTTTT TGTTTTTTTG TTTTTTTTTA AGAGAAACAT TTATAACTGG ATAGCATTGC    1920

AGTGAAAGCA GCTTGGGATG TTGGAGCTAA TGCCAGCTGT TTATACTGCT CTTTCAAGAC    1980

AGCCTCCCTT TATTGAATTG GCATTAGGGA ATAAACAAGC CTTTAAACGT GATAAAAGAT    2040

CAAAAACCTG GTTAGACATG CCAGCCTTTG CAAGGCAGGT TAGTCACCAA AGACTAACCT    2100

CCAAGTGGCT TTATGGACGC TGCATATAGA GAAGGCCTAA GTGTAGCAAC CATCTGCTCA    2160

CAGCTGCTAT TAACCCTATA ATGACTGAAA TGACCCCTCC ACTCTATTTT TGTGTTGTTT    2220

TGCACAGACT CCGGAAAAGT GAAGGCTGCC AATCTGAGTA GTACTCAAAT GTGAGGAACT    2280

GCTGGTCTTG GATTTTTTTT CCATTAAATT CAGCTGATCA TATTGATCAG TAGATAAACG    2340

TAAATAGCTT CAAATTTTAA AAGTGGAATT GCAGTGTTTT TTCACTGTAT CAAACAATGT    2400

CAGTGCTTTA TTTAATAATT CTCTTCTGTA TCATGGCATT TGTCTACTTG CTTATTACAT    2460
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TGTCAATTAT GCATTTGTAA TTTTACATGT AATATGCATT ATTTGCCAGT TTTATTATAT          2520

AGGCTATGGA CCTCATGTGC ATATAGAAAG ACAGAAATCT AGCTCTACCA CAAGTTGCAC          2580

AAATGTTATC TAAGCATTAA GTAATTGTAG AACATAGGAC TGCTAATCTC AGTTCGCTCT          2640

GTGATGTCAA GTGCAGAATG TACAATTAAC TGGTGATTTC CTCATACTTT TGATACTACT          2700

TGTACCTGTA TGTCTTTTAG AAAGACATTG GTGGAGTCTG TATCCCTTTT GTATTTTTAA          2760

TACAATAATT GTACATATTG GTTATATTTT TGTTGAAGAT GGTAGAAATG TACTATGTTT          2820

ATGCTTCTAC ATCCAGTTTG TACAAGCTGG AAAATAAATA AATATAACAT AAAAAAAAAA          2880

AAAAAAAAAA                                                                 2890
```

(2) INFORMATION FOR SEQ ID NO: 151:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2399 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

```
GAACTTTTCC ATCTGGCAAA CCGGAAACTC CATCCCCATT AAACCAACTC CCCCTTTTGG          60

TTTCCCCCCC AGNGGAATAG AATTTGGACN CCCATATAAA TCCAGGAAAC CACCTAAATT         120

CTTTAGTNGT TTGTGTTTGC AAGATCTAAG GTCATGGTAA ACATTAAGTT CTTAAAATTT         180

TTGGGAGGGA CCAGTGCACC TCTCCCTCTG AATTGTTCNC CAATTTAAAA TTGGAGTAAG         240

GTTTTAAAAT GTCTNATTCC ATTGGAAGGG TNTGTTATTT CATTTTGAGC CCAGAGGGGA         300

GAGGCACATT TTAAATATCA GAATTAGATT AGCTTTGAGT TTGTACAATT GGGAACATAA         360

TAGATTTTCA TAAATTATGT GTGCCTTGTT GGAAGTGTCA ACTGTCTTTA TGTCTGCTTG         420

TAAAAGTTTC AAAATATGTT TTCCCTCAAA AAGGCAACGT TACTTCATTT GCTTGAATAT         480

TATGATAGGA ATGCTTACTG ATATTACTTG ATAGTCATAT ATAGCCTAGG AAATTTAACA         540

TATATATAAC TATAGCAGTA TTAATAATGA TAGTTGTACT TCTTTAAAAC ATTAAATTTG         600

AGGAAACTTT AATGCTGTCT CGTGTACATT GCTTTACTAC AGTGAGGGGG AATATCCTTT         660

AGATTGAGCC TCAATTTACT GGTTAGTAGT ATGTGAACTC TGGTATAAAA ACGTAAACTA         720

GACAGTAGAG CCGATGAATT AAAATTGTAA ATTGCTACAT TGGCATTTTC TACCTCCTTT         780

TCTGTCAGAG TATTACTTTT TCCAGCATTT ATTCTTATTT GTGAGTAAAG AGGAAATGGG         840

AACCTGAGGT TAAAATTGAC ATTTTTGTTT CATTGAGAAT TTAAGCAGTA GGTACAGGAG         900

AAGTGACTTG TCACATTAAT TTGGTGCCTA AATCTGTAAC TACAAGTTGT GATCGACATG         960
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TACAAAATGT CTAAGAAAGG TCATATGCTG AATATTTTAC TTTTCCTGTA TAGTCTGCAT    1020

GATTTGTTTC ATAAACCCAG CTTATTTCCT CCAAAAAGCA AAATGGTCCT GTAATTTTTA    1080

AAGTAAAATA AACGTGCCAT TTTGTCTGCA ATCTATAATT TCAGGAAGTT ATTGRAAGTT    1140

CTGACTCAGG GCTTTTTAAC AGTTCAAGCA ATTGTCAGTT ATATTTTGGA AACTCCATCT    1200

GTGTAATTCT CCAGTGCCTT GAAAGAATTA TTAACTTGGC AACACTATTA AAACTTTATA    1260

AAAGATGGTC TTTAGTGCAC GTGTATCATT ATATACACGT TTTAAAGTCA TATTGCTTAG    1320

CTTGTTAATA ATGATTCTGC ATGTGTGCTG GGTTTGGGTA ATTCTTTAAA GGAAGTTTTC    1380

TAGATTTGCA CTTGATGTTT GTTTTTTAAA AACTGATTAT TTATGGCCGT GACACTGTTA    1440

CCAGAAAAGT AATTCTAATT AAGTTATTAT GCAAAGTCAT CTATAAGTAG CATCTGGGAA    1500

GAGGAGATSG AGGCCACAGT TTGCTATTTT AGTATGAAAG GAGGATCTGT TTGGGAAACA    1560

TAGATTGTCT TCCCCTCAAA TGAGGGGAAA AAAAAAGACC CTTTGTTCAA ATGGATTCTG    1620

TTGTAAAAAA TTATTTTTAA AGGAAATCAC AAATTGTATG TCATTCTTAA TGCTAGTCTT    1680

ATAGAATAAA TCCATAAAAT TGTTTTTATG TTCAGTATGT TTATGTCATT CTAAATGCAG    1740

CAAATTCAAT GATAGCAGTT CAATTGACTC ATAGCAGTGT TTTGTATTTT TTCTAATTCT    1800

TTAGCTTTCA ATATTGGATT AAAGTCTTGT TTGTGAATAT AGTTTCCGTA TGGCAAATGA    1860

TTTCTTGCTT ATTAGCTTTT GTTAAAGAAT GCTTAGTAAG AGCTAAGCTT TTAAAAGTAA    1920

TGCAAACATT TATCGTTAAT AAAACCTATG GTGTAATATC ATATAATGCT TTTCTTTGAT    1980

CTTTGGAGAA TTATTCTTTT ATAGTAGTAT ACATGAATTT TGATTTTTAA AGCATTTAAA    2040

AACAAATCTC AATACATTAA AAAACCTGTT ATTGTTAAAA RGGAAATTAC CATGCCTTTA    2100

AGAAACAAGG ATGTACATCT TCAATTCAGC ATRAGTGTCC ACATCTAGAA GGCTCTCATT    2160

GCAGTTGTTT ACAGTTAAGG TACCTCTATC TAAAGGGCCA AAGAAGCATT TCATAYTTTA    2220

ACACCTCACA TTCTTTCAGG ATTAAGACAT ATGAAAATAG TCTGAATAGG ATAAATTTGG    2280

ATAGGAAGTA ACTTAACCAG TCTGGGAAGA TTCAGGCTTT TTCTATKAAA AAGCTTATTC    2340

CTCTTCACAA CTCNGGTGGT AGGNTTTCAT TTTTCAAGAG GGTAGATATT TTAAAGCCA     2399
```

(2) INFORMATION FOR SEQ ID NO: 152:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 802 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

```
CGTGCCTGTA GTAAGCTCAT CCCTGCCTTT GAGATGGTGA TGCGTGCCAA GGACAATGTT      60

TACCACCTGG ACTGCTTTGC ATGTCAGCTT TGTAATCAGA GATTNTGTGT TGGAGACAAA     120

TTTTTCCTAA AGAATAACWT GAYCCTTTGC CARACGGACT ACGAGGAAGG TTTAATGAAA     180

GAAGGTTATG CACCCCMGGT TCGCTGATCT ATCAACATCA CCCCATTAAG AATACAAAGC     240

ACTACATTCT TTTATCTTTT TTGCTCCACA TGTACATAAG AATTGACACA GGAACCTACT     300

GAATAGCGTA GATATAGGAA GGCAGGATGG TTATATGGAA TAAAAGGCGG ACTGCATCTG     360

TATGTAGTGA AATTGCCCCA GTTCAGAGTT GAATGTTTAT TATTAAAGAA AAAAGTAATG     420

TACATATGGC TGGATTTTTT TGCTTGCTAT TCGTTTTTGT GTCACTTGGC ATGAGATGTT     480

TATTTTGGAC TATTGTATAT AATGTATTGT AATATTTGAA GCACAAATGT AATACAGTTT     540

TATTGTGTTA CCATTTGTGT TCCATTTGCT YCTTTGTATT GTTGCATTTA GTACAATCAG     600

TGTTTAAACT TACTGTATAT TTATGCTTTC TGTATTTACC AGCTATTTTA AATGAGCTGT     660

AACTTTCTAG TAAAGAATTG AAAAGCAAAT CCTCACTAAA GGATACACAG GATAGGATAA     720

AGCCAAGTCN CATCAACATT AAAAAATACT AAAANANAAA ACACAAAAAA AAAAAANCCC     780

GGGGGGGGCC CGGAACCCAT TC                                             802
```

(2) INFORMATION FOR SEQ ID NO: 153:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH:-461 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

```
CTAGGAGCAC CGAGCAGCTT GGCTAAAAGT AAGGGTGTCG TGCTGATGGC CCTGTGCGCA      60

CTGACCCGCG CTCTGCNCTC TCTGAACCTG GCGCCCCCGA CCGTCGCCGC CCCTGCCCCG     120

AGTCTGTTCC CCGCCGCCCA GATGATGAAC AATGGCCTCC TCCAACAGCC CTCTGCCTTG     180

ATGTTGCTCC CCTGCCGCCC AGTTCTTACT TCTGTGGCCC TTAATGCCAA CTTTGTGTCC     240

TGGAAGAGTC GTACCAAGTA CACCATTACA CCAGTGAAGA TGAGGAAGTC TGGGGGCCGA     300

GACCACACAG GTGGGAACAA GGACAGGGGG ATTTAAGCAG TCAAAAGGAA AAACATGTTA     360

AGACCCTAGA CTTGTATATT GACACACTTG TACCTTGTAA GGCAGAGGAA TGTAATTAAA     420

AAGCACTTAT TTGGCWNAAA AAAAAAAAAA AAAAAAAAAA C                        461
```

60

(2) INFORMATION FOR SEQ ID NO: 154:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2388 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

```
GCCCACGCGT CCGAAAGCGG AGAACGCTGG TGGGCCTGTT GTGGAGTACG CTTTGGACTG        60

AGAAGCATCG AGGCTATAGG ACGCAGCTGT TGCCATGACG GCCCAGGGGG GCTGGTGGCT       120

AACCGAGGCC GGCGCTTCAA GTGGGCCATT GAGCTAAGCG GGCCTGGAGG AGGCAGCAGG       180

GGTCGAAGTG ACCGGGGCAG TGGCCAGGGA GACTCGCTCT ACCCAGTCGG TTACTTGGAC       240

AAGCAAGTGC CTGATACCAG CGTGCAAGAG ACAGACCGGA TCCTGGTGGA GAAGCGCTGC       300

TGGGACATCG CCTTGGGTCC CCTCAAACAG ATTCCCATGA ATCTCTTCAT CATGTACATG       360

GCAGGCAATA CTATCTCCAT CTTCCCTACT ATGATGGTGT GTATGATGGC CTGGCGACCC       420

ATTCAGGCAC TTATGGCCAT TTCAGCCACT TTCAAGATGT TAGAAAGTTC AAGCCAGAAG       480

TTTCTTCAGG GTTTGGTCTA TCTCATTGGG AACCTGATGG GTTTGGCATT GGCTGTTTAC       540

AAGTGCCAGT CCATGGGACT GTTACCTACA CATGCATCGG ATTGGTTAGC CTTCATTGAG       600

CCCCCTGAGA GAATGGAGTT CAGTGGTGGA GGACTGCTTT TGTGAACATG AGAAAGCAGC       660

GCCTGGTCCC TATGTATTTG GGTCTTATTT ACATCCTTCT TTAAGCCCAG TGGCTCCTCA       720

GCATACTCTT AAACTAATCA CTTATGTTAA AAAGAACCAA AAGACTCTTT TCTCCATGGT       780

GGGGTGACAG GTCCTAGAAG GACAATGTGC ATATTACGAC AAACACAAAG AAACTATACC       840

ATAACCCAAG GCTGAAAATA ATGTAGAAAA CTTTATTTTT GTTTCCAGTA CAGAGCAAAA       900

CAACAACAAA AAAACATAAC TATGTAAACA AGAGAATAAC TGCTGCTAAA TCAAGAACTG       960

TTGCAGCATC TCCTTTCAAT AAATTAAATG GTTGAGAACA ATGCATAAAA AAAGTTGCAC      1020

AAGTTCCTTA TTTTCCTTAA TATTTCACTT CTATTTAATA CAAGCTGGGA CATAAAAATT      1080

CTGTTGGGGA TACCTGGGGG AAGATGTGAG AAACTAATGC TGAATTCAGC TTATACATGA      1140

TGAAAAGAAA AACCAGACAA AAGGAGCACA TAAATATGCA TACAGTGTAA CTGTTATTAT      1200

TTTAATACCC ACGATAAGGG ATTTTTGTTA GCATGTTTAG GGGGAACGAG GATTGGTGGG      1260

ATCCTTGGGG CCACAGGAAT CTGAGGCAAC GGAAGATATA TAGAGTGATC GTCCCCCTGC      1320

CGAAGGAACC TGGCAYCTGT CAAGCAGATG CTGCAGTTCA AACTTCAGCT TTTAAGATAG      1380

ATAGCTATTG AAGGCAGAGG GTCAGCAGGA GGATGTGTAT TTCTAATCTA CCCTGGTAAA      1440
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GTCATAGGTA AGACTCAAAA GCGGGATCTT ATTCAAAAGG CAGGTATTTC CTTTGTTTTC    1500

TGTCTTGAAA TAGCCCCTTC CCCTAAGGTG CATTCTCTCA AGTTTTCAGT ATTGCTTTAT    1560

TTGCAGTGAT TAAAAGAGAT GAGAGACTTT GGAGACAGAC AACGTAAGCA ACACATACAC    1620

ACATGAAATA CTCTAGACAG AGATGAATAT AAATCTGGCC TAATAACCAG TTTTCCATGT    1680

AACAGTGATT TTGTGTTTCG GGCTGAAGCA GTGGTTATAT TAAAAGCCAC TAATTCCCTT    1740

ATCCCTTTAA AAGATTTTTA CAATTCTCCA ACCACAAACA GCACTTCTAA AACTAACTTT    1800

ACTTTCTGCC CATAATTTGT TCTACATGGA AAAAAAAAAT ATTACTTTGG CCAGGGGTGT    1860

GTGTAAATGT GGCAGAATTC CTAGGCAGGC TGACCTTTAC AGTATGGGCC TTTAAGATAC    1920

TGGATCCTGG TTGGGCAACA AGTGTCACGC CTGAAGTTTC TGAAAACAAA TTAGAAGACT    1980

GTTGGCTTGG CTAATCTCGT AGTTCAGGGC CAAGTTTCTG TAGTCAGAAT GAAGAATAAA    2040

ATTGAAAGAA AAAGGGGGAA ATGCTTATAC TTGGCATTAA GTTGAATGCC TCAAGTCTTA    2100

ACTATGGCTT TGTAGATGAG GCAAAAGATT TCTTAGTGGT AAAATTTCTT CAACAGGTCA    2160

ATGCCAATCT GTATGCCATT TTAGTAAAGT AGGTAAGGAG AGTAGCCGCT CAGTAACTTT    2220

GGCACTAAAG AAAGAGTGTG GCTCTAGAAC TTCCAATCCC ATTGCTAGAT GTGCCCTTTA    2280

AAAGATGGTC CAGTGCTTTC AGGGAAGGAT GTTTAGCCAG TTTTCCTAGT ATTTGTTCCT    2340

TAAGATTTTT TGACCTGTGC TTAATAAGAC GGACGCGTGG GTCGACCC                2388
```

(2) INFORMATION FOR SEQ ID NO: 155:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 642 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

```
AAAACAGACC ATTTAAAAAC TCAGACAAGA TTATATTTAA TATATTAATT ACTAAAAAGG     60

CACAAGATTA CACTGAACAT ATTAGCTACT AAAAAGGCAC TGCTAAGACA TTCAAGCAAA    120

TAGCTATTAC ACACTACTGC AGATTTTACA GGTTTCTAAT TCTAACATAT GTTTGAAAAA    180

TCCGTGAGTA TTCCAAAATA TATTTAATAA TGGAATATCT GCATTAATAT ACCATCCATG    240

TGTTTTTACC ATTTGCCTTA ATATTGAATA TACTGTTTAC CTCACACTAA AAAGAAAACC    300

AGAAGCCTTA TTTGTGATTT TGGGAGTGGA AGCTTCCATT TTTGTGTCAA AAATGAATCC    360

TGATTCTTAT GGAAATCTCT GTTATTAAGA TATTTCAAGA TGAGACAACA CTGAAGATCA    420

AATTGTGTTT AGTATCACTA TCTTCTCTCC TCGTTTCTCT CTTACTCCTC ATCCTCCCAG    480
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```
AATCTACCAG TTTATGGTAG AAAGATGGGA ACCTTATTTG AATGTGTTTT TTTTTTTCCA      540

TGATGTCCAA TTTTGTTGTG GGAAAGGATT TGGATAAAAT TTTTGTTTAA ATTTTGGTAG      600

ATTTTTATCT ATACAAATTT AAATAAAATT ATGTTTTGTA AG                         642
```

(2) INFORMATION FOR SEQ ID NO: 156:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1251 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

```
GCCGCTGCCC CTCCACGGAG TTGCTGATCA TCTGGGCTGT GATCCACAAA CCCGGTTCTT       60

TGTCCCTCCT AATATCAAAC AGTGGATTGC CTTGCTGCAG AGGGGAAACT GCACGTTTAA      120

AGAGAAAATA TCACGGGCCG CTTTCCACAA TGCAGTTGCT GTAGTCATCT ACAATAATAA      180

ATCCAAAGAG GAGCCAGTTA CCATGACTCA TCCAGGCACT GAGCATATTA TTGCTGTCAT      240

GATAACAGAA TTGAGGGGTA AGGATATTTT GAGTTATCTG GAGAAAAACA TCTCTGTACA      300

AATGACAATA GCTGTTGGAA CTCGAATGCC ACCGAAGAAC TTCAGCCGTG GCTCTCTAGT      360

CTTCGTGTCA ATATCCTTTA TTGTTTTGAT GATTATTTCT TCAGCATGGC TCATATTCTA      420

CTTCATTCAG AAGATCAGGT ACACAAATGC ACGCGACAGG AACCAGCGTC GTCTCGGAGA      480

TGCAGCCAAG AAAGCCATCA GTAAATTGAC AACCAGGACA GTAAAGAAGG GTGACAAGGA      540

AACTGACCCA GACTTTGATC ATTGTGCAGT CTGCATAGAG AGCTATAAGC AGAATGATGT      600

CGTCCGAATT CTCCCCTGCA AGCATGTTTT CCACAAATCC TGCGTGGATC CCTGGCTTAG      660

TGAACATTGT ACCTGTCCTA TGTGCAAACT TAATATATTG AAGGCCCTGG GAATTGTGCC      720

GAATTTGCCA TGTACTGATA ACGTAGCATT CGATATGGAA AGGCTCACCA GAACCCAAGC      780

TGTTAACCGA AGATCAGCCC TCGGCGACCT CGCCGGCGAC AACTCCCTTG GCCTTGAGCC      840

ACTTCGAACT TCGGGGATCT CACCTCTTCC TCAGGATGGG GAGCTCACTC CGAGAACAGG      900

AGAAATCAAC ATTGCAGTAA CAAAAGAATG GTTTATTATT GCCAGTTTTG GCCTCCTCAG      960

TGCCCTCACA CTCTGCTACA TGATCATCAG AGCCACAGCT AGCTTGAATG CTAATGAGGT     1020

AGAATGGTTT TGAAGAAGAA AAAACCTGCT TTCTGACTGA TTTTGCCTTG AAGGAAAAAA     1080

GAACCTATTT TTGTGCATCA TTTACCAATC ATGCCACACA AGCATTTATT TTTAGTACAT     1140

TTTATTTTTT CATAAAATTG CTAATGCCAA AGCTTTGTAT TAAAAGAAAT AAATAATAAA     1200
```

ATAAAAAAAA AAAAACCCCG GGGGGGGCCC GGTCCCCAAT TGGCCCTATG G   1251

(2) INFORMATION FOR SEQ ID NO: 157:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2127 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

CCGGCGGGAG AGGGAAGCTG CAGCGAGAGG CGCGGATCTC AGCGCGGGAG CAGTGCTTCT   60

GCGGCAGGCC CCTGAGGGAG GGAGCTGTCA GCCAGGGAAA ACCGAGAACA CCATCACCAT   120

GACAACCAGT CACCAGCCTC AGGACAGATA CAAAGCTGTC TGGCTTATCT TCTTCATGCT   180

GGGTCTGGGA ACGCTGCTCC CGTGGAATTT TTTCATGACG GCCACTCAGT ATTTCACAAA   240

CCGCCTGGAC ATGTCCCAGA ATGTGTCCTT GGTCACTGCT GAACTGAGCA AGGACGCCCA   300

GGCGTCAGCG CNCCCTGCAG CACCCTTGCC TGAGCGGAAC TCTCTCAGTG CCATCTTCAA   360

CAATGTCATG ACCCTATGTG CCATGCTGCC CCTGCTGTTA TTCACCTACC TCAACTCCTT   420

CCTGCATCAG AGGATCCCCC AGTCCGTACG GATCCTGGGC AGCCTGGTGG CCATCCTGCT   480

GGTGTTTCTG ATCACTGCCA TCCTGGTGAA GGTGCAGCTG GATGCTCTGC CCTTCTTTGT   540

CATCACCATG ATCAAGATCG TGCTCATTAA TTCATTTGGT GCCATCCTGC AGGGCAGCCT   600

GTTTGGTCTG GCTGGCCTTC TGCCTGCCAG CTRACACGGC CCCCATCATG AGTGGCCAGG   660

GCCTAGCAGG CTTCTTTGCC TCCGTGGCCA TGATCTGCGC TATTGCCAGT GGCTCGGAGC   720

TATCAGAAAG TGCCTTCGGC TACTTTATCA CAGCCTGTGC TGTKATCATT TTGACCATCA   780

TCTGTTACCT GGGCCTGCCC CGCCTGGAAT TCTACCGCTA CTACCAGCAG CTCAAGCTTG   840

AAGGACCCGG GGAGCAGGAG ACCAAGTTGG ACCTCATTAG CAAAGGAGAG GAGCCAAGAG   900

CAGGCAAAGA GGAATCTGGA GTTTCAGTCT CCAACTCTCA GCCCACCAAT GAAAGCCACT   960

CTATCAAAGC CATCCTGAAA AATATCTCAG TCCTGGCTTT CTCTGTCTGC TTCATCTTCA   1020

CTATCACCAT TGGGATGTTT CCAGCCGTGA CTGTTGAGGT CAAGTCCAGC ATCGCAGGCA   1080

GCAGCACCTG GGAACGTTAC TTCATTCCTG TGTCCTGTTT CTTGACTTTC AATATCTTTG   1140

ACTGGTTGGG CCGGAGCCTC ACAGCTGTAT TCATGTGGCC TGGGAAGGAC AGCCGCTGGC   1200

TGCCAAGCTG GNTGCTGGCC CGGCTGGTGT TTGTGCCACT GCTGCTGCTG TGCAACATTA   1260

AGCCCCGCCG CTACCTGACT GTGGTCTTCG AGCACGATGC CTGGTTCATC TTCTTCATGG   1320

CTGCCTTTGC CTTCTCCAAC GGCTACCTCG CCAGCCTCTG CATGTGCTTC GGGCCCAAGA   1380

409

```
AAGTGAAGCC AGCTGAGGCA GAGACCGCAG AGCCATCATG GCCTTCTTCC TGTGTCTGGG    1440

TCTGGCACTG GGGGCTGTTT TCTCCTTCCT GTTCCGGGCA ATTGTGTGAC AAAGGATGGA    1500

CAGAAGGACT GCCTGCCTCC CTCCCTGTCT GCCTCCTGCC CCTTCCTTCT GCCAGGGGTG    1560

ATCCTGAGTG GTCTGGCGGT TTTTTCTTCT AACTGACTTC TGCTTTCCAC GGCGTGTGCT    1620

GGGCCCGGAT CTCCAGGCCC TGGGGAGGGA GCCTCTGGAC GGACAGTGGG GACATTGTGG    1680

GTTTGGGGCT CAGAGTCGAG GGACGGGGTG TAGCCTCGGC ATTTGCTTGA GTTTCTCCAC    1740

TCTTGGCTCT GACTGATCCC TGCTTGTGCA GGCCAGTGGA GGCTCTTGGG CTTGGAGAAC    1800

ACGTGTGTCT CTGTGTATGT GTCTGTGTGT CTGCGTCCGT GTCTGTCAGA CTGTCTGCCT    1860

GTCCTGGGGT GGCTAGGAGC TGGGTCTGAC CGTTGTATGG TTTGACCTGA TATACTCCAT    1920

TCTCCCCTGC GCCTCCTCCT CTGTGTTCTC TCCATGTCCC CCTCCCAACT CCCCATGCCC    1980

AGTTCTTACC CATCATGCAC CCTGTACAGT TGCCACGTTA CTGCCTTTTT TAAAAATATA    2040

TTTGACAGAA ACCAGGTGCC TTCAGAGGCT CTCTGATTTA AATAAACCTT TCTTGTTTTT    2100

TTCTCCATGG AAAAAAAAAA AAAAAAA                                        2127
```

(2) INFORMATION FOR SEQ ID NO: 158:

   (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 1625 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

```
CAAAAGATCT ATAATCAGGA CATTGTTTAT GTAAGTTGGA CAANAAAAAT TCTTCCCCTT     60

TATGTCCACC CTTCCTATGA TTGCAAGACA AAATTTCCCT CCTTTACCTC ATCCCTATAA    120

CATGGGAGGC TGAGAAAAAT GAGGGGAGAT GGAACCAGAT ACAAGGAGAT CCAATAAGAG    180

AAGCTTATTT AAATATTGTG AAATAAAGGA AGAMCCAAAG CATTTTTTTA AGTGGGGAAT    240

CCTTTTGAAC AGTTATTATT TATCCATATT ATTAAYAACA TCTTTTCTGA CAAAATCCAT    300

CAGATGAAGT GTAAATGGAT AATCTTTTAA TGGATCTAAA CCTAGAAAGT TTCACTTACT    360

GTTCATGTCC GTGTTCCAGA ATTGTGAAAT GGTGTGTGGT TTTGCTTTCC AAGTTCTTCT    420

CTGCCTCCTC TTAATTCTCT AATTCCATGT CTTACAGAAG AATGAGAAAT TTCTTTCTTA    480

CTTGAGTATC ATGCTCTAAA AAACTTGGCT TCAGTCACAG AAACGCTGGC TCTCCTGTGC    540

TTATATTGAA GCCAACTGCC TTTAATTCTT GGGCCCTCTT ATATTTTTAA GGTGCAAAAT    600
```

410

TTGAAGTCTC AGTCACCAGA CACAGGTTCT ATACAATTAA TGATGAGCTG GAGAAGTAAT   660

ATGTAGCTAA TTTTTCAAAA GCATTGAATA TACTTTCCGG AAAGAAAACA GAAATTAAAT   720

ATTGCCACAT CTTGCCAGAA TCCCATCTGA CACCTTAACT TTGTCAGGTT TCCTACAACT   780

TGCTAATCAA GTTTTATACA TTCTAAATCT CCCCAGTTTC TTTGGGGCTG GAAGATGCAA   840

CTTCCATTTA ATAGAAACTT TGAAATCTTG GGGTAAGGGA GCAGTGGGGG GACTAGGGAG   900

AAGGATAAGA AATAGAATTA TTGAAAAGCC CCCACCAGGG ACCTTCCTGG CCAGAATATG   960

CAGAGTAATT CCTGCTGGCT TCACCTTTGA AAGTCCCTCG AAACTATGCA GATGAAACTG   1020

AGTCTGTTTT TGATATTGTC AGATGTATTC TACCTTGGAA GTCCCNACAC CTAAACTGGA   1080

ATTCTTGTAT TTACATCTCC TCCACTGTCC CCCACACCAC CCCTCAATTC CTGCTGCCCC   1140

TGCTAATGTT AAGCATTTTT CTCTTGTTAT CATCAGGTTC ACATTAAAAM CAGRTACTTA   1200

CAAACTGACT TGAAGCACAG ATACTTTTAC GAATGTGATA AAATATTTTC TTAAGAAAAG   1260

GAAAGAGGAT GTGGGTCAAA TAAAACACCG CATGGATGTT GATTGGTGAA TACTGGTGTA   1320

AGAAAAGGGA GCTCAGGAAT TTTTATTACT GTATTTGTAA ATGAGTTTGA AGGAATTTGT   1380

AAATGCCACT GGTACATTTT TAAGGTGACA CATTTGCTCC TTATAAAGTT ATTAAAAATT   1440

ACAGGGTAAG CTTAAATGAC GTTTGCCAGT AGTTTTACTT TATATAATCA ATATTGATAT   1500

TGTTGCTGAA CTATGTAACT TTATGATGCA TTTTTCAGTC CCTTTTCAGA GCAAATGCTT   1560

TTGCAATGGT AGTAATGTTT AGTTTAAATT GACTTAATAA ATTMTTACCT GAGCAAAAAA   1620

AAAAA   1625

(2) INFORMATION FOR SEQ ID NO: 159:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1687 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CGGGGTCACC AGTTATTAGA GGAAGTAACA CAAGGGGATA TGAGTGCAGC AGACACATTT   60

CTGTCCGATC TGCCAAGGGA TGATATCTAT GTGTCAGATG TTGAGGACGA CGGTGATGAC   120

ACATCTCTGG ATAGTGACCT GGATCCAGAG GAGCTGGCAG GAGTCAGGGG ACATCAGGGT   180

CTAAGGGACC AAAAGCGTAT GCGACTTACT GAAGTGCAAG ATGATAAAGA GGAGGAGGAG   240

GAGGAGAATC CACTGCTGGT ACCACTGGAG GAAAAGGCAG TACTGCAGGA AGAACAAGCC   300

AACCTGTGGT TCTCAAAGGG CAGCTTTGCT GGGNATCGAG GACGATGCCG ATGAAGGCCC   360

411

```
            TGGAGATCAG TCAGGCCCAG CTGTTATTTG AGAACCGGYG GAAGGGACGG CAGCAGCAGC      420

            AGAAGCAGCA GCTGCCACAG ACACCCCCTT CCTGTTTGAA GACTGAGATA ATGTCTCCCC      480
     5
            TGTACCAAGA TGAAGCCCCT AAGGNAACAG AGGCTTCTTC GGGGACAGAA GCTGCCACTG      540

            GCCTTGAAGG GGAAGAAAAG GATGGCATCT CAGACAGTGA TAGCAGTACT AGCAKTGAGG      600

    10      AAGAAGAGAG CTGGGAACCC TCCGTGGTAA GAAGCGAASC GTGGGCCTAA AGTCAGATGA      660

            TGACGGGTTT GAGATAGTGC CTATTGAGGA CCCAGCGAAA CATCGGATAC TGGACCCCGA      720

            AGGCCTTGCT CTAGGTGCTG TTATTGCCTC TTCCAAAAAG GCCAAGAGAG ACCTCATAGA      780
    15
            TAACTCCTTC AACCGGTACA CATTTAATGA GGATGAGGGG GAGCTTCCGG AGTGGTTTGT      840

            GCAAGAGGAA AAGCAGCACC GGATACGACA GTTGCCTGTT GGTAAGAAGG AGGTGGAGCA      900

    20      TTACCGGAAA CGCTGGCGGG AAATCAATGC ACGTCCCATC AAGAAGGTGG CTGAGGCTAA      960

            GGCTAGAAAG AAAAGGAGGA TGCTGAAGAG GCTGGAGCAG ACCAGGAAGA AGGCAGAAGC     1020

    25      CGTGGTGAAC ACAGTGGACA TCTNCAGAAC GAGAGAAAGT GGCACAGCTG CGAAGTCTCT     1080

            ACAAGAAGGC TGGGCTTGGC AAGGAGAAAC GCCATGTCAC CTACGTTGTA GCCAAAAAAG     1140

            GTGTGGGCCG CAAAGTGCGC CGGCCAGCTG GAGTCAGAGG TCATTTCAAG GTGGTGGACT     1200

    30      CAAGGATGAA GAAGGACCAA AGAGCACAGC AACGTAAGGA ACAAAAGAAA AAACACAAAC     1260

            GGAAGTAAGC AGAGCTGCCA GGCTCCCAGG AGAGCATGGG GACTAGGAGG AAGGGTGTGG     1320

            CATGGCTCAG TCTGGCCCCC TTGATTACCG GCCTAGCCCC TGCTCACATC ACAGCTGTCT     1380
    35
            GAAGAACAGT GAGGTGGAGT GCCTAGAACT CCCGTGGTGG TCCTGAGCAG AGAGGAGGAT     1440

            GTCCTCCTGC CTGCCTGAAG GTCTCCCATG AAAACACTGC TGAACTGTGT TGACACTCAT     1500

    40      GACCCTTTTT TTAAACCGTT AAAGGGAAGT TCGGTGTTGG AGCGATACTC AATGTAGTCA     1560

            GTCTACACCT GGACGTGTGG GCCACTTAAG CCCTCCCCAC CCCCATCCTA TTCCTRAATA     1620

            AAACCAGGAT AATGGAARAA AAAAAAAAAA AAAAAAAAAG GGGGGCCCN TAAAGGGNCC     1680
    45
            CANNTTT                                                            1687
```

50

(2) INFORMATION FOR SEQ ID NO: 160:

        (i) SEQUENCE CHARACTERISTICS:
55   (A) LENGTH: 1842 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:
60

```
   GGATGACAGA TTGCGACANA GATTTGTGAC CCTTCCTGCT GAACTTCAGA GGGAGCTGAA     60

   ANCAGCGTAT GATCAAAGAC AAAGGCAGGG CGAGAACAGC ACTCACCAGC AGTCAGCCAG    120

 5 CGCATCTGTG CCCCGAGAAT CCTTTACTTC ATCTAAAGGC AGCAGTGAAA GAAAAGAAAA    180

   GAAACAAGAA GAAAAAAACC ATTGGTTCAC CAAAAAGGAT TCAGAGTCCT TTGAATAACA    240

   AGCTGCTTAA CAGTCCTGCA AAAACTCTGC CAGGGGCCTG TGGCAGTCCC CAGAAGTTAA    300
10
   TTGATGGGTT TCTAAAACAT GAAGGACCTC CTGCAGAGAA ACCCCTGGAA GAACTCTCTG    360

   CTTCTACTTC AGGTGTGCCA GGCCTTTCTA GTTTGCAGTC TGACCCAGCT GGCTGTGTGA    420

15 GACCTCCAGC ACCCAATCTA GCTGGAGCTG TTGAATTCAA TGATGTGAAG ACCTTGCTCA    480

   GAGAATGGAT AACTACAATT TCAGATCCAA TGGAAGAAGA CATTCTCCAA GTTGTGAAAT    540

   ACTGTACTGA TCTAATAGAA GAAAAAGATT TGGAAAAACT GGATCTAGTT ATAAAATACA    600
20
   TGAAAAGGCT GATGCAGCAA TCGGTGGAAT CGGTTTGGAA TATGGCATTT GACTTTATTC    660

   TTGACAATGT CCAGGTGGTT TTACAACAAA CTTATGGAAG CACATTAAAA GTTACATAAA    720

25 TATTACCAGA GAGCCTGATG CTCTCTGATA GCTGTGCCAT AAGTGCTTGT GAGGTATTTG    780

   CAAAGTGCAT GATAGTAATG CTCGGAGTTT TTATAATTTT AAATTTCTTT TAAAGCAAGT    840

   GTTTTGTACA TTTCTTTTCA AAAAGTGCCA AATTTGTCAG TATTGCATGT AAATAATTGT    900
30
   GTTAATTATT TTACTGTAGC ATAGATTCTA TTTACAAAAT GTTTGTTTAT AAAGTTTTAT    960

   GGATTTTTAC AGTGAAGTGT TTACAGTTGT TTAATAAAGA ACTGTATGTA TATTTGGTAC   1020

35 RGGCTCCTTT TKGTGAAYCC TTAAAAACTC AACTCTAGGA RGCAACTACT GTTTATTATA   1080

   CTAAARGGCT GAAAAMCCTC CAGGCCAGAC TGCTAAGCTC TGAAATYCCT GAGAGGTCTC   1140

   AGACCGGGAT TCTACTTGTT CCAAGAAAGG GTAAAGCTTC TAAACCATCT TATTCTTGTC   1200
40
   TCCAAGCATG AACACAGGAG CATGTYAAGA AAATCTTTAC TACTTTCTYC CATGCGGAGA   1260

   AATCTACATA TTTTGAATTA GAAACACCCT CACACCCACT TGAAGATTTT TTTCCTGGGA   1320

45 ACATTATGTC CCGTAGATCA GAGGTGGTGT TGTCTTTTTG CTTCTACTGG CCATTGAGAA   1380

   ACTTTGATGA TAAAAAAGAA CGGTATAGAT TTTTCAAACG TATATAAAAT ATTTTTATGT   1440

   TATATGTTAT GCCATAACTT TAAAATAAAA ATAGTTTAAA ATTCTATGCT AGTGGATATT   1500
50
   TGGAACTTTT TCCTCAAACA AACACCCCAC ACTGACTTCA GCAAAACCCT AAAACTAGCT   1560

   ACAGATTACT ACTACGAATG AATCATYAAG TTTTGTGTCT GCAACAATTT AGAAGCACTA   1620

55 AGCCCAAATA TCAGGAAATG TGTGTATGAT GGAATTTTCT AGGACAAAAC AGATCAAGAT   1680

   TAAAACAGGA TCAAGGATTA ATGGTATAAA AATGGTCTAC TAAAACAGGA TCAAGGATTA   1740

   AAACAGGATC AAGGATTAAT GGTATAAAAA TCTCTACTGG TTACCGGGTG GCNGGGCCAT   1800
60
```

ACAGGGTAGT GGTGGATGGA TAGTTTAGTT TGGNAAGGGT AA   1842

5

(2) INFORMATION FOR SEQ ID NO: 161:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 770 base pairs
10
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:
15

GGCACGAGCC CTATGCTGTT CTTGTGATAA TGAGTGAGTC TCACAAGATC TGGTGGTGTT   60

ATAGGCATCT GGCATTTCCC CTGCTGACGC TCATTCTCTA TCCTGCCACC CTGGGAAGAA   120

20 GTGTCTTCTG TCATGATTGT AAGTTTCCTG AGGCCTCCCC AGCTATGTAG AACTGTGAGC   180

CAATTAAACC TCTTTTCTCT ATAAATTATC CAGTCTTATA TATTTCTTCA TAGCAGTGTG   240

AGAACAGATA ATACCGTAAA TTGGTATCAC AGAGAGTGGG GTGTTGCTAT AAACACATCT   300
25

GAAAATGTTA AAGCAAATTT GGAACTGGGT AACAGGCAAA GGCTGGAACA GTTKGAAGAA   360

CAGTTAAGAA GAAGACAGGA AAATATGAGA AATCTTGAAA CTTCCTAGAG TCTTAAAGGT   420

30 CTCAGAAGAC ATGAAGATGT GGGAAGCTTT GGAACTTCCT AGAGACTTGT TTGAATGGCT   480

TTGACCAAAA TGCTGATAGT GATATGGACA ATGAAGTCCA GGCTGAGCTT ATCCAGACAG   540

ACATAAGAAG CTCGCTGGGA ACTTGAGTAA AGATCACTCT TGCTAGGCAA AGAGACTGGT   600
35

GGCCTTTTTT CCTCTGCCCT AGAGATCTGT GGAAATCTGA ACCTGAGAGA GATGATTTAG   660

GGTATCTGGC AGAAGAAATA TCTAAGCGGC AAAACCTTCM AGAGGAAGCA GAGCATAAAC   720

40 GTTTGAAAAA TTTGCAGCCT GACNATGGGA GACCAAAGTT AAACCCAATT   770

45 (2) INFORMATION FOR SEQ ID NO: 162:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 519 base pairs
        (B) TYPE: nucleic acid
50
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

55 GAATTCGGCA CGAGCTGAGA GGCACAGGAG CAACAGCCAG TGCCCCCTGC AGAGGACCAC   60

TGGGGTCACA GACTTCARAC CTGATGACCT GGGCTCAGAT CCCAGCTCTG CACCTACCAG   120

CCGTGTGACA AGGTGTCCTC TCTGAGCCTC AGTCACACAC TGCCTTAACG GTTGGGCCTC   180
60

414

```
ATGGAGCTGT TTGTGAAGGT TAAATGGGAA GACATAAAGC ACTTAGCCCA GAGCCAAGGA      240

CATGCTGAAT AGGATAATGG TGGCCTCCTT TGGCGCTGTG CTGGTGCAGG TGTGCCGAGG      300

AAYTGGGCAG GGGTGACAGA TACCTCTTCT AACCTAGTTC CTTTCCAAGA ACCTAATTGG      360

TGTCTCTCCC TCCCCCAGGC AATTGGAAGG AGGAGGCTGG GCCCCAGCCC CAGAATACGG      420

GAGGTTTCTC ACCGTGGTAG GGAAATTGCT GGGTTGGGGG TGTGGGCAAC CACAGTGATC      480

GTCTCTCTGC AGGACGGATG AGGCTTTGCT GACAGAGGC                             519
```

(2) INFORMATION FOR SEQ ID NO: 163:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 753 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

```
GGCACGAGCG GCACGAGCAG CCAGTTGCTG ACTGGCACAT GGCCTCCAGC GTCCCGGCTG       60

GTGGGCACAC TAGAGCCGGA GGGATCTTCT TAATTGGTAA ATTGGATCTT GAAGCTTCAC      120

TGTTTAAATC TTTTCAGTGG CTTCCCTTTG TACTTAGAAA AAAATGCAAC TTCTTCTGCT      180

GGGACTCATC CGCTCACAGC CTTCCCCTCC ACCCTCTCTC TGCCTCATGC TCTGCCCCTG      240

CCTGCCATGC CTCCGATACT CACCTTTTGT ACCCCAGCAC CCGTGCCCTC TGCCCCTCGA      300

TCTTTGCCTG GCTGGTTGCT CCTCACTCAG TGTTCAGGAC AAATGCTCCT GGCCCTACCC      360

CATCTAGCCA GTCTAGCCCG GTCTTCCCTG TCTTCCCTGT TTCATTCATG GCTCTTATTG      420

TTTGTTWACT TGTGTGCTGT TGACTTTTAA CTCTCTCAGT CCCCACTGGA ATGCAAGCGA      480

TCTCCCAAGC TCCTAGAATT GTTCCTGCCT CTTCACAGGC CCTTACGCTG TGTGTGCTCG      540

TGCCGAATTC GGCACGAGGG TATGTGCACT TGCTGGTATG TATGTAGGTG TTTGCTAACA      600

CATACGTGCA CACGCAGAAT GCTTCCAGGG GACTGCACAG CCTCTAGTTC GCAGCCCCCA      660

CCCCTCCCTT TGSCCCTGCA CTCTCCCCTC TCTGAGCTGC ATTCGCATGA AAGGGTGCAN      720

GGTTCCTGAN CCCGCNAGCG NCACCTCCTG GGA                                  753
```

(2) INFORMATION FOR SEQ ID NO: 164:

       (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1400 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double

415

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

```
GGCACAGTTT ATTAATACCT ATTATGGGAA AGTCACTTTG GTTGGCATTG AAAATTACAT        60

CATCTTTAAA GCAGTATTTG TCCCCAGATG GACTCATCAC TAGCAAAGAC TAGGTTCATT       120

GGAAGGCATA GGGTGAGAGA ATGGGAAGAT GRAGTGGAGG CGGGTTGTTA AAGTGCTGTC       180

AGTGAGTGAT TTTGTCTACT TGAATAATGG TCCATGTTTG GGGGCATATT GTGTTTCATA       240

AGAAGTGAAA GGTATTTGCA AAGTAAGCTA CAAATGACCC ATAAATCTGT TAACAACAGT       300

CCTTAATATG CAAAGATGAA AAACAAGCAT TACTGCTACC CAAAGGGAAC TGGTGCTTGG       360

TGATGTGCAG ATGGGGCTGT TGGTTAAGAG AGCTATTACA GGTTTTCTCT CTTAGGTTTC       420

ATAGGAGGTA GTTACTGAGA TGAGATTGTT TTATCTTTTT GAATACAGAT CTCTTGTCTT       480

GAGTTAGTTC TGAGGATGGG AGTAATAAAG GAGTTTTTTG TTTTTTTGTT TGTTGTTTG       540

TTTTGGCTCC TTAGTAATAC TCCTCTGACA TTTATTTCTA TTATTCTTCA AAGAAAGGAA       600

ACCAACTGAA ATGTTTGCTT TAACAAACAT TTTAATAAGT TCTCTGGGTT TTTTTTTCCC       660

CTTTTAAAAA AATTAGCATA TACCATAGCA ATAAAGAAC TAATGTTAAC TATTGTATGC       720

TACAACTTAA GTGATTTTTC TAAAGAAGCA CAATGTCATT GRAAGTATTA TTGAAAAGGA       780

TCATAGTCAC ATTGAATTTG TGAAGGCCAA AGAAATTGAA GGGAGTGATA TTTTCATTTT       840

ATGATATTCA CATATTTAGT AAATTTTGTG TACAAGAATA CCAGGCAGAG TGTTTTACCC       900

ATGGAAACAG GTTTCAGATT ACTTTGTTTT TACTGTTAGA GTCTCAAGTT TAGAAATGCT       960

AACACTTAAA TCAGTTTTTT TCTCACTATA CTTGAAGATT GTTAATATTT TGATATCTTC      1020

CTAGCTTGAT GGAATTTAAA CATATCTTCA GATCTGTGAC AGTGACAGCC AATAGGACTG      1080

ATAATATTAG CTTCAAACCA ATAATATCCA GGGTTAAAAT AAAAATCATA GTGAAAGTAC      1140

GATTGTAAAA TTATGCTATA TTAACTTTTA AGTCTGTAAT AACTTGACAT CAAAATGTTA      1200

TGTAATTACC ATAAATAATG GCTAGCGAGA ACATCTTTGG AAATTCTCAA ATTACCTTTC      1260

TTACTACACT GTTTGCAGAA TGAATGTAGA AATGATCCTG TTAGCTTTCT GAATGTTCTG      1320

TGGTTGAATG TGTTTTTGCT TAAATAAAGC TTTTGGTATT TGTTTAAATW ACAAAAAAAA      1380

AAAAAAAAAA AAAAACTCGA                                                  1400
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(2) INFORMATION FOR SEQ ID NO: 165:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2153 base pairs
          (B) TYPE: nucleic acid

416

```
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:
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```
CAGGCCTCAG GGCCTCTGGT GGCTCTGGCC CAGACAGTAT TTGCAGTTCT TGTGCTATGG        60

GTGGGAGTCT TCTTCCTCAA GTTTCGGCAG CTGTGCTGTG NCTGGATGGG CTGCTCCTCC       120

CAGGGCTCAA GGGCTGTGGT CCGCTCAGGG TCTCATTTCC CCAGGCCAAG TTCAAGGCAG       180

CAGCCCTTTG TGAGGCGCTC TTGGCCCTGG GCTGGAGGGA GAACTTTAAG CTTTTTTGCT       240

CACAGGGACG TGGTATGGGC CCTGGGTGCA GGTGCCCACA TTCTGCTAAT GAGAGCTTTG       300

TCTGATCAGT CCTGGGTCCA TCAGTTTGTC CATGTGTCCG CTGCCAGCC CGTCCCTTGG        360

GATCCTTCCC CTGGGGTGTA GCCTTGTTCA TTAGTATATA CTCATTCCTT CATGCTTTCC       420

TCAGCAGAAC ACTTCCACTT CTGAGGTGAG CTTTTGCCCC RTGCCCTTCC TCCACAGGTG       480

TTGCCTTTTT ATAAAGACCT GATAGCAGAA TAAATTGGTG TTTCCCTGTT GACCCAGCAC       540

CATTTCTGTG GGCCTAGAAT ATGGCCCTCA ACCCTTAGAG TGGGGCAGTG AGGGCTTGAG       600

GAGTGACCCT TCCTTTCTCA TGGTTTTAGT CATTTTGGCT GCCAGCCCTT AATGGCACAG       660

ATCTGCTGCT TCTAACAGAT GGCCAGGAGG TGACACCGAT TTCAGCCATT GCCAAGGTTA       720

GCACCCTCTC CTTTGAGCCT AGGGCCACAC TGTTCATTGT CACTTTAGGC AAGTGCCTGT       780

TTGGCTTTAA AGGTAAGCCT GCCAGCTGTG AGAAGCCTTG GTAACTGATG GACTCATTTC       840

CTGGTCCTTA AAGATGCAGC CTCTTAAGGG CTCCTTGATG GATGCCATCT CTCCTAGCCC       900

CCAGCCCTGG TGCCACTGGT GGGCAGGTTC CCATTCTTTG GGGCTGGGAG GGACAGCTTG       960

CCTGTTTCTG GTCACAAATT ACAGTCTTCT CTCCTGTACC ATTCTGTGGC TTCAGCATGG      1020

GGGCAGTAGC CTTTCATTAG TGTAGATAGT CATTCCCTGG TAGGGTGGAG GGTAAGACAT      1080

AGGGTCTGGA ACTGTTTGGG ACCTTTTGGG GATGTCCTGT GCCTCCCAGA TTCCTMGATT      1140

CTGGGAGGAG AGGCTGCCGC ATTCTGCTGC TCCTCACAGC GAGCAAAGCT GCACCCACTT      1200

ACATTCAGTA TTTTCCTGGC ACTACAAAGA GTGGGAAGGC CTGGGATTTG CTGCTGCTCC      1260

CTTAGAGCAG GGCCCCTYTT TTCAGCACTT TGGACACCTG GAGACCCAGC CCTGTTATTT      1320

AATGGTAGTG GGCAAGTGTG TGTGCATACT GTCTGCCACT GCTTTCTCCC TGCCCCATGC      1380

CAGAGAGCCC TGTCCCTGCC AGGCCCAGCC TTCTTAGCCC CAACTTGGGA ACAAAGTGCA      1440

ACATGGGATC ATGGGTTGGG GTGCTCAGGT GAGCCCTCTC TATAGTGCTT CCCTGGGCCA      1500

AGCTGACACC AGCCCCTGAG GGTGGGGTGG GACGGGTGGT GCTTAAAAGA GGAAGGGGAC      1560

CAGTGTAGCA ACTTGCCAGG GACCCCACCC CTCCCTCTCT GGGCCTGTGC AGTGAGCATG      1620

GGGATTCCCA TCAAGGGGCC TGGCACCTGT GCTAGTTACG TAGCCGCTGN TCACGCGCTC      1680
```

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ACTCCTGACC ACATGCACGT TCCCTAGATG CAGACTGCTT TGAACTTTAA AGCTGTACAA        1740

TTTGGTTATG TTTGTGCTGA CTTAAAATAT ATTTTAATGA GGAAAAAATA ATGGAGAACC        1800

CTGGGAAGGA CCTGGTTCTT TTGCTTCTCG GGGAACTGTA AGCCCTCGCG TTCTGGGAAT        1860

CGCTCTCTGC TGCTCTTTCC TGGAAGCTAA GCCTGTCTCC ACCGCCCGAG GCCTGCGCCG        1920

GTGCTCCCGC CGCAGTTGCG TTTGCTTTGG ACCTTGCGTG CGGGGGAGGG GGTGCTCGGT        1980

CCGAGCCCGC TCCTTTCTGT ACACCTAGCG CTGCCCGCCC CGCTTGTGTC TGAGGTCGTG        2040

TATGTCAAAA ATAAAGCCGC TAGAAACGGA AAAAAAAAA AAAAAAAAA AAAAAAAAA          2100

AAACTCGAGG GGGGGCCCGT ACCCAATTAA CCCNNTATGA TCTATAAAGC GTC              2153
```

(2) INFORMATION FOR SEQ ID NO: 166:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1251 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

```
GCCCACGCGT CCGCCCACGC GTCCGGCGGT GCGGAGTATG GGGCGCTGAT GGCCATGGAG         60

GGCTACTGGC GCTTCCTGGC GCTGCTGGGG TCGGCACTGC TCGTCGGCTT CCTGTCGGTG        120

ATCTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGGAGCGCA        180

CTAGAGTTTA ACTGGCACCC AGTGCTCATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC        240

GCCATCATCG TCTACAGACT GCCGTGGACC TGGAAATGCA GCAAGCTCCT GATGAAATCC        300

ATCCATGCAG GGTTAAATGC AGTTGCTGCC ATTCTTGCAA TTATCTCTGT GGTGGCCGTG        360

TTTGAGAACC ACAATGTTAA CAATATAGCC AATATGTACA GTCTGCACAG CTGGGTTGGA        420

CTGATAGCTG TCATATGCTA TTTGTTACAG CTTCTTTCAG GTTTTTCAGT CTTTCTGCTT        480

CCATGGGCTC CGCTTTCTCT CCGAGCATTT CTCATGCCCA TACATGTTTA TTCTGGAATT        540

GTCATCTTTG AACAGTGAT TGCAACAGCA CTTATGGGAT TGACAGAGAA ACTGATTTTT         600

TCCCTGAGAG ATCCTGCATA CAGTACATTC CCGCCAGAAG GTGTTTTCGT AAATACGCTT        660

GGCCTTCTGA TCCTGGTGTT CGGGGCCCTC ATTTTTTGGA TAGTCACCAG ACCGCAATGG        720

AAACGTCCTA AGGAGCCAAA TTCTACCATT CTTCATCCAA ATGGAGGCAC TGAACAGGGA        780

GCAAGAGGTT CCATGCCAGC CTACTCTGGC AACAACATGG ACAAATCAGA TTCAGAGTTA        840

AACAGTGAAG TAGCAGCAAG GAAAAGAAAC TTAGCTCTGG ATGAGGCTGG GCAGAGATCT        900
```

```
ACCATGTAAA ATGTTGTAGA GATAGAGCCA TATAACGTCA CGTTTCAAAA CTAGCTCTAC       960

AGTTTTGCTT CTCCTATTAG CCATATGATA ATTGGGCTAT GTAGTATCAA TATTTACTTT      1020

AATCACAAAG GATGGTTTCT TGAAATAATT TGTATTGATT GAGGCCTATG AACTGACCTG      1080

AATTGGAAAG GATGTGATTA ATATAAATAA TAGCAGATAT AAATTGTGGT TATGTTACCT      1140

TTATCTTGTT GAGGACCACA ACATTAGCAC GGTGCCTTGT GCAKAATAGA TACTCAATAT      1200

GTGAATATGT GTCTACTAGT AGTTAATTGG ATAAACTGGC AGCATCCCTG A              1251
```

(2) INFORMATION FOR SEQ ID NO: 167:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 882 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

```
GACSMTCTAG AACTATGGTC CCCCGGGACT GCAGGAATTC GGCACAGCGG CTGCGGGCGC       60

GAGGTGAGGG GCGCGAGGTT CCCAGCAGGA TGCCCCGGCT CTGCAGGAAG CTGAAGTGAG      120

AGGCCCGGAG AGGGCCCAGC CCGCCCGGGG CAGGATGACC AAGGCCCGGC TGTTCCGGCT      180

GTGGCTGGTG CTGGGGTCGG TGTTCATGAT CCTGCTGATC ATCGTGTACT GGGACAGCGC      240

AGGCGCCGCG CACTTCTACT TGCACACGTC CTTCTCTAGG CCGCACACGG GCCGCCGCT       300

GCCCACGCCC GGGCCGGACA GGGACAGGGA GCTCACGGCC GAYTCCGATG TCGACGAKTT      360

TCTGGACAAK TTTCTCAGTG CTGGCGTGAA GCAGAGTGAC YTTCCCAGAA AGGAGACGGA      420

GCAGCCGCCT GCGCCGGGGA GCATGGAGGA GAGCGTGAGA RGCTACGACT GGTCCCCGCG      480

CGAMGCCCGG CGCACCCAGA CCAGGGCCGG CAGCARGCGG ANCGGAGGAR CGTGCTGCGG      540

GGCTTCTGCG CCAAYTCCAG CCTGGCCTTC CCCACCAAGG AGCGCGCATT CRACGACATC      600

CCCAACTCGG AGCTGAGCCA CCTGATCGTG GACGACCGGC ACGGGGCCAT CTACTGCTAC      660

GTGCCCAAGG TGGCCTGCAC CAACTGGAAG CGCGTRATGA TCGTGCTGAG CGGAAGCTGT      720

GCACCGCGTG CGCCTACCGC GACCCGYTGC GNTCCCGCGC GAGCACGTGC ACAACGCCAG      780

CGCGCACTGA CTTCAACAAT TCTGGCGCCG CTACGGGAAG TCTCCCCCAC CTCATGAAGT      840

CAAGCTCAAG AATACACCAA TTCTTTCTGC GCGACCCTTC TG                        882
```

(2) INFORMATION FOR SEQ ID NO: 168:

419

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1208 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

GGGAAACTCA AAAGGATGAT GGAATGGTTG ATGGAGCCAG AGCCTAGAAG TRAAGGGATA   60

CAGAGTGAAG ATAGAGGTAT TTACGTATAT TTWAATATTA GCTTTGGAAT TACGTAGGGA   120

TTCTTAAGAA AAGATCATGA CAGGACAGCC ACATTTGGTA AAATGTCAGG GCAGCCAGTG   180

CATGGTCCTC CTGGGGCTCC TCAGTTGACG GGTTTAAATC ATTTCCTGAT CCCCCTGCCC   240

TGGTTTGAGG AATGCATACA GTACGTGAAA TGCCTGTGGT ATGAGTTGCA ATGGGCAATC   300

AACCTGGGTA AATCCAAGAT TAATGATTAG TTCTAAAGAT CCAGTTGAAG TTCTAGAGTG   360

GGAATTTTCC GTCAAGCARC TCAGCACAGC TTTATGCCTG TTCCTCTAAT AACGATAGGT   420

AACAAATAGC TGTGTKTWCA CAGCTAGGAR GATAACCAAA TCTAGAGTTC TTGARTCTCA   480

TTTAATAAAT AAKTATTATG AGTACCAACT GCATATTTCA GGCACTGCAT TTGACTCTGT   540

TAAATACTGA TYCCTTAKGA CMSCCACWTC AGAWAACMTT AATCTGTCTG ATCAATAAAC   600

AGCTTGACTT AGAGRGGTAA AATAGCTTGC CACAGGTWAC CCAATTAGTA GGTAACAGCG   660

ACAGAATAAC AGTGCAGTTA AAATCTTAGA CTGGAGACTA ATTGCATAAG TTTGAATTTC   720

AGTTCTGCTA TGTAAATTTG GGTGAGTACC TTAATTYACC TGAGTCTCGG TCTTTATATC   780

TGTAGAATGG AGCTAATGAT ATTACTTAAT TTGCTTTATG TGAGATTAAA TGTACTAATA   840

TATGTAAATC ACTTACAACA GCATTTGACA TATTTGACAT ACTTAATATA TTTGCTACTA   900

ATACTATTAG CAACAGCATT CTGATTTTCC AAGTTGAAAT TCAGTGTTTT CTTTTTTACT   960

TTGCCATAAT TTACAATGTT GTGCTCTGTA AACCATAAAT TTCCCTGAGG TGTTGTCAGG   1020

TTAAAAAAAA ATCACTATGG CCCCCARNMA CTTGGAAAAT AGAAATGAGA CCAGCTTCAT   1080

CTATATTCTT TACTGCAAAT AACTTAGAAT TGTAATAGGC TAATATGTAC TGGGACTTCC   1140

AATTTGGGAA TATGACAAAA ATAATACTAT TTAGCTAAAA CATATACAGA ACTTATTTTT   1200

CCTCTGAA   1208

    (2) INFORMATION FOR SEQ ID NO: 169:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1307 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

```
GGCACGAGAG AAAAGAGGTT GAGAATGTTT TCTAGCAGGC AGAATGTGCA TACATGTTTT        60

CATGARTGTC CTTTGGGTGC TGTTTCTTTT AAATCCTCTG TGCACAGGGC TCTGGCCTTT       120

ARTAAACTGT TTTTCTGTCT TACGTCATGC TGACTGGGTG CTAGGGGCTG ATTACAAAGG       180

GGAAGAGTTG AACAGACATC AGGGGCCGAT GAAACCAAAG GACTAGGAGT CAGGAGAACA       240

AGTCAGGGAT TAGGAGACAG CGGTTTGGTT TATTGTTATC CAGCTGGAGG ACTCCTAGGG       300

GCAGCAGCAG GAGGAATACC AGGGCCACGG AGGGGCAGGA GTCTCACAGT GGAGGGCAGA       360

CTCTAACAGA TGCCAGCTGA ACGCTCGCTG GCCCTGGATG TCATACGAGT TGGGGACCAG       420

AAATCTGGGC TCAGAGAACC CGTCCAGGGA GATTTGAAGC CATGGGTTAT CTTCTAGAGT       480

TGATACTGAT AATATATTTT AATTTTTATT GATGTTTAAT ACCTTCTGAA ACAGGAGGGT       540

AAGATCAGAT GGGAAGCCCY TCTGTTGAAG GATCTTGGGA ACCTTGGTGG TTTTTTTTTT       600

TTGGTTTTTT TTTTTTTGAT CGAGCTGTGG ACATCCTTCT TAATTCGATT NTGAGGATTT       660

GTTTAACTAA AAAGTTCCCA AACACAGAAA GGGCCTCCCC ACCTGCTTTG GGGAGCTGTC       720

TGTSCTGGGA GTGCCAGGCA TCCSATGGGA CCCATCACTG CCAGTGTCTG TGCCTCCCAG       780

AGGTCAGCCC TGTGTCTGCC CTGGCTCTGT CTCCTCTGTG ACAGGGCAGA GCATTTCTGG       840

TCAGTTTCTC CATGGTGCCT CCCACCCCTT TGTAAAGTGG ATGGACATGA TGGAATTCAG       900

TTGTCTCACC CTGATAGCCT GGGTGTTGAT ATTCACTTTA CCCGCACTCA GACACAGGCG       960

ACCTTGAAGC AGTTCTCGGT GTGTAGAGTC CACGTGACAG TCCCCACAGC CTCCCCAGAT      1020

AGCTGTGTGC CTGTGCGCTA CTGCTGTGCC ATTTTCCCAA CTTNGGCGTT TCACTAAATG      1080

CAGCTGATCT CTCTCTCTGT GCACTCGTGA TCCATGTTGA ACAATACATG TAGGTTCTTT      1140

TTCCACGCAA TGTAAGAACA TGATATACTG TACGTTGGAA AGCATTTACC TTATTTATAT      1200

ACCTGAATGT TCCTACTACA CAAATAAACA TATATTAAAT WCTAAAAAAA AAAAAAAAAA      1260

CTGGAGGGGG GGCCCGGTAC CCAAATCGCC GGATAGTGAT CGTAAAC                    1307
```

(2) INFORMATION FOR SEQ ID NO: 170:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1624 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

```
     GGCACGAGGT CGCCGCCGCG GCCGCCTGGA ATTGTGGGAG TTGTGTCTGC CACTCGGCTG     60

     CCGGAGGCGA AGGTCCCTGA CTATGGCTCC CCAGAGCCTG CCTTCATCTA GGATGGCTCC     120

 5   TCTGGGCATG CTGCTTGGGC TGCTGATGGC CGCCTGCTTC ACCTTCTGCC TCAGTCATCA     180

     GAACCTGAAG GAGTTTGCCC TGACCAACCC AGAGAAGAGC AGCACCAAAG AAACRGAGAG     240

     AAAAGAAACC AAAGCCGAGG AGGAGCTGGA TGCCGAAGTC CTGGAGGTGT TCCACCCGAC     300

10   GCATGAGTGG CAGGCCCTTC AGCCAGGGCA GGCTGTCCCT GCAGGATCCC ACGTACGGCT     360

     GAATCTTCAG ACTGGGAAA GAGAGGCAAA ACTCCAATAT GAGGACAAGT TCCGAAATAA     420

15   TTTGAAAGGC AAAAGGCTGG ATATCAACAC CAACACCTAC ACATCTCAGG ATCTCAAGAG     480

     TGCACTGGCA AAATTCAAGG AGGGGGCAGA GATGGAGAGT TCAAAGGAAG ACAAGGCAAG     540

     GCAGGCTGAG GTAAAGCGGC TCTTCCGCCC CATTGAGGAA CTGAAGAAAG ACTTTGATGA     600

20   GCTGAATGTT GTCATTGAGA CTGACATGCA GATCATGGTA CGGCTGATCA ACAAGTTCAA     660

     TAGTTCCAGC TCCAGTTTGG AAGAGAAGAT TGCTGCGCTC TTTGATCTTG AATATTATGT     720

25   CCATCAGATG GACAATGCGC AGGACCTGCT TTCCTTTGGT GGTCTTCAAG TGGTGATCAA     780

     TGGGCTGAAC AGCACAGAGC CCCTCGTGAA GGAGTATGCT GCGTTTGTGC TGGGCGCTGC     840

     CTTTTCCAGC AACCCCAAGG TCCAGGTGGA GGCCATCGAA GGGGGAGCCC TGCAGAAGCT     900

30   GCTGGTCATC CTGGCCACGG AGCAGCCGCT CACTGCAAAG AAGAAGGTCC TGTTTGCACT     960

     GTGCTCCCTG CTGCGCCACT TCCCCTATGC CCAGCGGCAG TTCCTGAAGC TCGGGGGGCT     1020

35   GCAGGTCCTG AGGACCCTGG TGCAGGAGAA GGGCACGGAG GTGCTCGCCG TGCGCGTGGT     1080

     CACACTGCTC TACGACCTGG TCACGGAGAA GATGTTCGCC GAGGAGGAGG CTGAGCTGAC     1140

     CCAGGAGATG TCCCCAGAGA AGCTGCAGCA GTATCGCCAG GTACACCTCC TGCCAGGCCT     1200

40   GTGGGAACAG GGCTGGTGCG AGATCACGGC CCACCTCCTG GCGCTGCCCG AGCATGATGC     1260

     CCGTGAGAAG GTGCTGCAGA CACTGGGCGT CCTCCTGACC ACCTGCCGGG ACCGCTACCG     1320

45   TCAGGACCCC CAGCTCGGCA GGACACTGGC CAGCCTGCAG GCTGAGTACC AGGTGCTGGC     1380

     CAGCCTGGAG CTGCAGGATG GTGAGGACGA GGGCTACTTC CAGGAGCTGC TGGGCTCTGT     1440

     CAACAGCTTG CTGAAGGAGC TGAGATGAGG CCCCACACCA GGACTGGACT GGGATGCCGC     1500

50   TAGTGAGGCT GAGGGGTGCC AGCGTGGGTG GGCTTCTCAG GCAGGAGGAC ATCTTGGCAG     1560

     TGCTGGCTTG GCCATTAAAT GGAAACCTGA AGGCCAAAAA AAAAAAAAAA AAAAAAAAAA     1620

55   AAAA                                                                  1624
```

60   (2) INFORMATION FOR SEQ ID NO: 171:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 2003 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GGCACGAGCC AGCTTGCAGG AGGAATCGGT GAGGTCCTGT CCTGAGGCTG CTGTCCGGGG   60

CCGGTGGCTG CCCTCAAGGT CCCTTCCCTA GCTGCTGCGG TTGCCATTGC TTCTTGCCTG   120

TTCTGGCATC AGGCACCTGG ATTGAGTTGC ACAGCTTTGC TTTATCCGGG CTTGTGTGCA   180

GGGCCCGGCT GGGCTCCCCA TCTGCACATC CTGAGGACAG AAAAAGCTGG GTCTTGCTGT   240

GCCCTCCCAG GCTTAGTGTT CCCTCCCTCA AAGACTGACA GCCATCGTTC TGCACGGGGC   300

TTTCTGCATG TGACGCCAGC TAAGCATAGT AAGAAGTCCA GCCTAGGAAG GGAAGGATTT   360

TGGAGGTAGG TGGCTTTGGT GACACACTCA CTTCTTTCTC AGCCTCCAGG ACACTATGGC   420

CTGTTTTAAG AGACATCTTA TTTTTCTAAA GGTGAATTCT CAGATGATAG GTGAACCTGA   480

GTTGCAGATA TACCAACTTC TGCTTGTATT TCTTAAATGA CAAAGATTAC CTAGCTAAGA   540

AACTTCCTAG GGAACTAGGG AACCTATGTG TTCCCTCAGT GTGGTTTCCT GAAGCCAGTG   600

ATATGGGGGT TAGGATAGGA AGAACTTTCT CGGTAATGAT AAGGAGAATC TCTTGTTTCC   660

TCCCACCTGT GTTGTAAAGA TAAACTGACG ATATACAGGC ACATTATGTA AACATACACA   720

CGCAATGAAA CCGAAGCTTG GCGGCCTGGG CGTGGTCTTG CAAAATGCTT CCAAAGCCAC   780

CTTAGCCTGT TCTATTCAGC GGCAACCCCA AAGCACCTGT TAAGACTCCT GACCCCCAAG   840

TGGCATGCAG CCCCCATGCC CACCGGGACC TGGTCAGCAC AGATCTTGAT GACTTCCCTT   900

TCTAGGGCAG ACTGGGAGGG TATCCAGGAA TCGGCCCCTG CCCCACGGGC GTTTTCATGC   960

TGTACAGTGA CCTAAAGTTG GTAAGATGTC ATAATGGACC AGTCCATGTG ATTTCAGTAT   1020

ATACAACTCC ACCAGACCCC TCCAACCCAT ATAACACCCC ACCCCTGTTC GCTTCCTGTA   1080

TGGTGATATC ATATGTAACA TTTACTCCTG TTTCTGCTGA TTGTTTTTTT AATGTTTTGG   1140

TTTGTTTTTG ACATCAGCTG TAATCATTCC TGTGCTGTGT TTTTTATTAC CCTTGGTAGG   1200

TATTAGACTT GCACTTTTTT AAAAAAAGGT TTCTGCATCG TGGAAGCATT TGACCCAGAG   1260

TGGAACGCGT GGCCTATGCA GGTGGATTCC TTCAGGTCTT TCCTTTGGTT CTTTGAGCAT   1320

CTTTGCTTTC ATTCGTCTCC CGTCTTTGGT TCTCCAGTTC AAATTATTGC AAAGTAAAGG   1380

ATCTTTGAGT AGGTTCGGTC TGAAAGGTGT GGCCTTTATA TTTGATCCAC ACACGTTGGT   1440

CTTTTAACCG TGCTGAGCAG AAAACAAAAC AGGTTAAGAA GAGCCGGGTG GCAGCTGACA   1500

GAGGAAGCCG CTCAAATACC TTCACAATAA ATAGTGGCAA TATATATATA GTTTAAGAAG   1560

423

GCTCTCCATT TGGCATCGTT TAATTTATAT GTTATGTTCT AAGCACAGCT CTCTTCTCCT   1620

ATTTTCATCC TGCAAGCAAC TCAAAATATT TAAAATAAAG TTTACATTGT AGTTATTTTC   1680

AAATCTTTGC TTGATAAGTA TTAAGAAATA TTGGACTTGC TGCCGTAATT TAAAGCTCTG   1740

TTGATTTTGT TTCCGTTTGG ATTTTTGGGG GAGGGGAGCA CTGTGTTTAT GCTGGAATAT   1800

GAAGTCTGAG ACCTTCCGGT GCTGGGAACA CACAAGAGTT GTTGAAAGTT GACAAGCAGA   1860

CTGCGCATGT CTCTGATGCT TTGTATCATT CTTGAGCAAT CGCTCGGTCC GTGGACAATA   1920

AACAGTATTA TCAAAGAGAA AAAAAAAAA AAAAAACTCG NGGGGGGGCC CGGTACCCAA   1980

TTCGCCCTAT AGTGAGCCNA TTC   2003

(2) INFORMATION FOR SEQ ID NO: 172:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 786 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

GGCACAGCGG CACGAGAAGA CTTTGGTGTT TAAGAGATTA ATGTGTTAGC CAGAACAACT   60

CATTTCTCTA CCMGTGTGTA GTCCATTTAT CTTTAAAGAT TTTCTATTGG AATAATTTTG   120

AAATTACTTT CTTAGTTTTC TTCATTAAAA ACTAAGAAAA TGCTTTGTTT ATTATGAATT   180

GCTATTTCTC TTGATTATTA TTCTTGGAGA AAGTCTATCA GACGTAATTC TTCTGATTTG   240

CTTCTAGGCT AGAGGAAAAT GTGAAAGATG ACAAATGAAA ATTTCAAAGG TTGTCAGTAG   300

TATGACTTCT TTTATCGTTT GTCATTATCA CAAATATATC AACATAGGAC TTTTAAAAGA   360

TATTTTGTAC ATATTGGGCC TTAGTAGGAT TTTGCATGAA TTTTTTTTTT CTTTTATGCC   420

CAGAGAGAAA GAGCAAAGAA ATAACCAAGG GTGATGTACT CGTATTGAAG GTTTACCAAA   480

TAAGGACTGC TTTTATTATG AACTATAGTC TATATTCTAA GTAAATCAAT TTTTCTATTA   540

TGTGTTTTTT GTTCCTGCAG GCAAGATCTC TGAACTTTAT GCAGAGGGTT CTTTTAAAAA   600

AACAAAGTTG AATTTTTTTA TTTCTTGGAA TATTTTTTTT CATTGATTTC TCCCAAGTAG   660

AGCAGATTCA AATCTCCTTT GTACCCTATG TCTTTTTTGT TTTGCTATTA GCTCAGTATT   720

CCGTTTCTAC ATTTTCCTTT CCTAGAACCA GTCAATAAAT GACAAAAAAA AAAAAAAAAA   780

ACTCGA   786

(2) INFORMATION FOR SEQ ID NO: 173:

    (i) SEQUENCE CHARACTERISTICS:

5
        (A) LENGTH: 1758 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

10
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

```
GGGACGAGCC CTGCCCACCT CCTGCAGCCT CCTGCGCCCC GCCGAGCTGG CGGATGGAGC       60

TGCGCACGGG GAGCGTGGGC AGCCAGGCGG TGGCGCGGAG GATGGATGGG GACAGCCGAG      120

ATGGCGGCGG CGGCAAGGAC GCCACCGGGT CGGAGGACTA CGAGAACCTG CCGACTAGCG      180

CCTCCGTGTC CACCCACATG ACAGCAGGAG CGATGGCCGG GATCCTGGAG CACTCGGTCA      240

TGTACCCGGT GGACTCGGTG AAGACACGAA TGCAGAGTTT GAGTCCAGAT CCCAAAGCCC      300

AGTACACAAG TATCTACGGA GCCCTCAAGA AAATCATGCG GACCGAAGCT TCTGGAGGCC      360

CTTGCGAGGC GTCAACGTCA TGATCATGGG TGCAGGGCCR GCCCATGCCA TGTATTTTGC      420

CTGCTATGAA AACATGAAAA GGACTTTAAA TGACGTTTTC CACCACCAAG GAAACAGCCA      480

CCTAGCCAAC GGTATTTTGA AAGCGTTTGT CTGGAGTTAG AAAGTTCTCT TCTTCAACAC      540

GTCCCTCCCC AGGGTGTTCC TCCCTGTGAC CCAGCCGCCT CGACTTCGGC CCGCTTGCTC      600

ACGAATAAAG AACTCAGAGT TGTGTGTGCA ATGCACACCC AGACACACGC ACGCACACAC      660

ACGCGCGCGC ACACACATGC TTTTTTCTGT TCCCCTCCGC TTTCTGAAGC CTGGGGAGAA      720

ATCAGTGACA GAGGTGTTTT GGTTTTATTG TTATGTGGGT TTTCTTTTGT ATTTTTTTTG      780

TTTGTTTTGT TTTTAAACAT TCAAAAGCAA TTAATGATCA GACATAGGAG AAACCCTGAA      840

TAGAAACAAA ACTTTTGAAT GCTGGATTCA AAAAAAAAA AAAGTTATCT GGACAGCTTC      900

TTTGAGACTA TTTAAAAACT GGTACAACAG GTCTCTACAA CGCCAAGATC TAACTAAGCT      960

TTAAAAGGTC AAGAAGTTTT ATGGCTGACA AAGGACTCGC GCAACGCAGA AGGCCTTTCC     1020

CACCTTAAGC TTCCGGGGAT CTGGGAATTT TACCCCCATT CTCTTCTGTT TGTCTGAGTC     1080

TCATCTCTCT GCAAGCAAGG GCTGAAATCA TTTTGTTTGG TTGTTTTGAG GGAGAGAGGC     1140

GGGGTGGGGG GGTGCAAATC TGCCAGCAGC TCTTACGTAA GGCATGTTTT ATTGGGGAGG     1200

GCTGAGCTTT TATTTTCTCC TCTCCAGTGG GGTTGGCTTT TATTGTTTCT TGTTTGGGTT     1260

TGGAATGGAA ATATGGATAG CAGCATAAAG TACTTTTATT TTGACAAAAT TCATTTTTTT     1320

CAACAATGGA GACATAGATT TGACCCACAA TAACTTCTCC CCCTCTCTTT TTACTCTGCT     1380

CAAAAAGCAT CTCTCCTCCC ATTACCCAAC CTTGGTCATA AGTGTGCCTG GCTGGTTTGC     1440

AGATATTTGT TCTGCTTTGT AAAAATTGGC CATTAGTGCA TTTATTGAGA TGATCTCTAA     1500
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    AGAGCTATGC CCTGACCTAC CCCTGATTCT ATGACATTGG GGCCCTTCTT TTGCTGAAAC    1560

5   TGCCTTACGT AATGGTTTTA CTCCTTGAAA GAGATTTGAC GGAATCCATT TTATGCCAAG    1620

    TGCTGCCCTG CACTGTTTCT GCAATATGTG GTGTATGCTG TGGTGATCTT GCTGGGAATG    1680

    ATTATAAGTG TGTGTGTGGT GGGGGAGTGG GTATTACATG CATTGCTGAA GAGTCAAAAA    1740

10  AAAAAAAAAA AAACTCGA                                                  1758
```

15 (2) INFORMATION FOR SEQ ID NO: 174:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 888 base pairs
              (B) TYPE: nucleic acid
20   (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

```
25  CTGTTAGAAT GCCCAGTTTA CCTGGATGGC AACCCAACAG TGCTCCTGCC CACCTGCCCC    60

    TCAATCCTCC TAGAATTCAG CCCCCAATTG CCCAGTTACC AATAAAAACT TGTACACCAG    120

    CCCCAGGGAC AGTCTCAAAT GCAAATCCAC AGAGTGASMC ACCACCTCGG GTAGAATTTG    180

30  ATGACAACAA TCCCTTTAGT GAAAGTTTTC AAGAACGGGA ACGTAAGGAA CGTTTACGAG    240

    AACAGCAAGA GAGACAACGG ATCCAACTCA TGCAGGAGGT AGATAGACAA AGAGCTTTGC    300

35  AGCAGAGGAT GGAAATGGAG CAGCATGGTA TGGTGGGCTC TGAGATAAGT AGTAGTAGGA    360

    CATCTGTGTC CCAGATTCCC TTCTACAGTT CCGACTTACC TTGTGATTTT ATGCAACCTC    420

    TAGGACCCCT TCAGCAGTCT CCACAACACC AACAGCAAAT GGGGCAGGTT TTACAGCAGC    480

40  AGAATATACA ACAAGGATCA ATTAATTCAC CCTCCACCCA AACTTTCATG CAGACTAATG    540

    AGCGAGGCAG GTAGGCCCTC CTTCATTTGT TCCTGATTCA CCATCAATCC CTGTTGGAAG    600

45  CCCAAATTTT TCTTCTGTGA AGCAGGGACA TGGAAATCTT TCTGGGACCA GCTTCCAGCA    660

    GTCCCCAGTG AGGCCTTCTT TTACACCTGC TTTACCAGCA GCACCTCCAG TAGCTAATAG    720

    CAGTCTCCCA TGTGGCCAAG ATTCTACTAT AACCCATGGA CACAGTTATC CGGGATCAAC    780

50  CCAATCGCTC ATTCAGTTGT ATTCTGATAT AATCCCAGAG GAAAAAGGGN AAAAAAAARA    840

    AMAARAAARA ARAAAGGAGA TGATGATGCA GAATTCCACC AAGGCTCC               888
```

55

    (2) INFORMATION FOR SEQ ID NO: 175:

60   (i) SEQUENCE CHARACTERISTICS:

426

```
     (A) LENGTH: 2379 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: double
     (D) TOPOLOGY: linear

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GGCAGAGCTA GTGTGGACTC CATCCCCCTG GAGTGGGATC ACGNCTATGA CCTCAGTCGG       60

GACCTGGAGT CTGCAATGTC CAGAGCTCTG CCCTCTGAGG ATGAAGAAGG TCAGGATGAC      120

AAAGATTTCT ACCTCCGGGG AGCTGTTGSC TTATCAGGGG ACCACAGTGC CCTAGAGTCA      180

CAGATCCGAC AACTGGGCAA AGCCTGGATG ATAGCCGCTT TCAGATACAG CAAACCGAAA      240

ATATCATTCG CAGCAAAACT CCCACGGGGC CGGAGCTAGA CACCAGCTAC AAAGGCTACA      300

TGAAACTGCT GGGCGAATGC AGTAGCAGTA TAGACTCCGT GAAGAGACTG GAGCACAAAC      360

TGAAGGAGGA AGAGGAGAGC CTTCCTGGCT TTGTTAACCT GCATAGTACC GAAACCCAAA      420

CGGCTGGTGT GATTGACCGA TGGGAGCTTC TCCAGGCCCA GGCATTGAGC AAGGAGTTGA      480

GGATGAAGCA GAACCTCCAG AAGTGGCAGC AGTTTAACTC AGACTTGAAC AGCATCTGGG      540

CCTGGCTGGG GGACACGGAG GAGGAGTTGG AACAGCTCCA GCGTCTGGAA CTCAGCACTG      600

ACATCCAGAC CATCGAGCTC CAGATCAAAA AGCTCAAGGA GCTCCAGAAA GCTGTGGACC      660

ACCGCAAAGC CATCATCCTC TCCATCAATC TCTGCAGCCC TGAGTTCACC CAGGCTGACA      720

GCAAGGAGAG CCGGGACCTG CAGGATCGCT TGTSGCAGAT GAATGGGCGC TGGGACCGAG      780

TGTGCTCTCT GCTGGAGGAG TGGCGGGGCC TGCTGCAGGA TGCCCTGATG CAGTGCCAGG      840

GTTTCCATGA AATGAGCCAT GGTTTGCTTC TTATGCTGGA GAACATTGAC AGAAGGAAAA      900

ATGAAATTGT CCCTATTGAT TCTAACCTTG ATGCAGAGAT ACTTCAGGAC CATCACAAAC      960

AGCTTATGCA AATAAAGCAT GAGCTGTTGG AATCCCAACT CAGAGTAGCC TCTTTGCAAG     1020

ACATGTCTTG CCAACTACTG GTGAATGCTG AAGGAACAGA CTGTTTAGAA GCCAAAGAAA     1080

AAGTCCATGT TATTGGAAAT CGGCTCAAAC TTCTCTTGAA GGAGGTCAGT CGTCATATCA     1140

AGGAACTGGA GAAGTTATTA GACGTGTCAA GTAGTCAGCA GGATTTGTCT TCCTGGTCTT     1200

CTGCTGATGA ACTGGACACC TCAGGGTCTG TGAGTCCCAY ATCAGGAAGG AGCACCCCAA     1260

ACAGACAGAA AACGCCACGA GGCAAGTGTA GTCTCTCACA GCCTGGACCC TCTGTCAGCA     1320

GTCCACATAG CAGGTCCACA AAAGGTGGCT CCGATTCCTC CCTTTCTGAG CCARGGCCAG     1380

GTCGGTCCGG CCGCGGCTTC CTGTTCAGAG TCCTCCGAGC AGCTCTTCCC CTTCAGCTTC     1440

TCCTGCTCCT CCTCATCGGG CTTGCCTGCC TTGTACCAAT GTCAGAGGAA GACTACAGCT     1500

GTGCCCTCTC CAACAACTTT GCCCGGTCAT TCCACCCCAT GCTCAGATAC ACGAATGGCC     1560

CTCCTCCACT CTGAACTAAG CAGATGCCAT CTGCAGAAGT GCTGGTAGCA TAAGGAGGAT     1620
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CGGGTCATAA GCAATCCCAA ACTACCAACA AGAGGACCTT GATCTTGGCG AAAGCCMTCG    1680

GTGTGGCAGC TTTAGCCTCC TCCAGATCAC ATGTGTGCAA ATTATGGCTT CAGAGGTGGA    1740

AGATAAACAG TGACGGGGGA ACAAACAGAC AACAAGAAGG TTTGGAAGAA ATCTGGTTTG    1800

AGACTCTGAA CCTTAGCACT AAGGAGATTG AGTAAGGACC TCCAAAGTTC CCCGGACTCA    1860

TGAATTCTGG GCCCTTGGCC NATTCTGTGC ACAGCCAAGG ACTTCAGTAG ACCATCTGGG    1920

CAGCTTTCCC ATGGTGCTGC TCCAACCATC AGATAAATGA CCCTCCCAAG CACCATGTCA    1980

GTGTCGTACA ATCTACCAAC CAACCAGTGC TGAAGAGATT TTAGAACCTT GTAACATACA    2040

ATTTTTAAGA GCTTATATGG CAGCTTCCTT TTTACCTTGT TTTCCTTTGG GGCATGATGT    2100

TTTAACCTTT GCTTTAGAAG CACAAGCTGT AAATCTAAAA GGCACTTTTT TTTAGAGGTA    2160

TAAAGAAAAA CTAGATGTAA TAAATAAGAT CATGGAAGGC TTTATGTGAA AAAAGTTGAA    2220

TGTTATAGTA AAAAAAAAAG ATATTTATGT ATGTACAGTT TGCTAAAGCC AAGTTTTGTT    2280

TGTATTGATT TCTTTGCATT TATTATAGAT ATTATAAAAT AAAAAAAAAA AAAAAAAAC     2340

TCGAGGGGGG GCCCGGTACC CAATTCGCCC TATAGTGAG                           2379
```

(2) INFORMATION FOR SEQ ID NO: 176:

  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 1348 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: double
    (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

```
GCGCCTTCAC GATGCCGGCG GTCAGTGGTC CAGGTCCCTT ATTCTGCCTT CTCCTCCTGC      60

TCCTGGACCC CCACAGCCCT GAGACGGGGT GTCCTCCTCT ACGCAGGTTT GAGTACAAGC     120

TCAGCTTCAA AGGCCCAAGG CTGGCATTGC CTGGGGCTGG AATACCCTTC TGGAGCCATC     180

ATGGAGGTGA GGGGCAGGGG TGGGGACCGC TATGCCCAGG GTCCCTCAAA GTGCTGGAGG     240

GGCTGTRACT TGGTGGGGAG TGGGTCTGTC ACAGCCATCC TCTGTCCAGG GTGGGGCAAG     300

GCCTGGGACA GTGCCAGGCA CCCCAGGACC CCTTCCAGGC TTGTCTCCTG CTCCACCGCC     360

TCAACACCCC CCACCCCTGC CCAAGCTGTT TCTCCTCTGC CTCTCTNNTT CCCTGCCCCA     420

GGACTTCTCT CTTCTCCTCT GCCTCTCCTT GGACCCCTGC CCTTCCTCTA CCTCTGACCT     480

GTGAACACAC AGACACATGC TCACACACTA AGTCCCARGC ACACMSAAAG GCAATGTGGA     540

CCAGCACAAA CCTCCACTCT CCCGGCTCCA TCCCARCGGG CCTGTGGCTG GCCATGAAAA     600
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428

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CTGGGGGCTA CCTGGAGGGA AGCATCCTCA TCCCAGGTGA GTGGGCACCA GCCCTTCCCT        660

GTATGTGTGT TGTGGGTGGA AGCAGGCATG AGAGCATCTT AGCCCATAGG TTTGTATTCA        720

GGGACTTCCA AACCCAGACC TACAAAGAGT GTGTCTTCTA CCAGATCTTG TTCAAAAAAG        780

GGTTTGTGAT GATGGAACTA CACGATAGAG GGAGTGAGCA AGAACAATGA GGATTAGAGT        840

GGAGCGTGAA ATAGTCTAGG AGCATGGCTT CCAAAACATA TGCTGTGAGG TCTGTCCACC        900

TGAGAGTTGG GCCATGGATT TAATTCTGAG CCTCTTAGCA GGCAAAGCAA AGACAGAAAG        960

CAGATCGGCT GTGGATTTCT GTCTATAAAA TGTGAGTTCT TGGCCGGGTG CGGTGGCTCA       1020

CGCCTGTAAT CCCGGCGCTT TGGGAGGCCA GGGCGGATGG TCGCGAGGT CAGGAGGTTG        1080

GAAACCATCC TGGCCGGAAT GGTGAAGCCC TGACTCTACT AGAAGTGCAA AGATTGGCTG       1140

GGTGTGGTGG CGTGCGCCTG TGGTCCCAGC TTCTCGGGAG GCTGAGGCGG GAGAGTTGCT       1200

TGGGCCTGGG AGGCCGAGGT TGCGGTGAGC TGAGATCCTG CCATTGCACT TCAGCCTGGG       1260

CACAGAGCCA GACTCTGGCT CAAAAAAAAA AAAAAAAAAA ACTCGAGGGG GGCCCGTACC       1320

CAATTCGCCG NATATGATCG TAAACAAT                                         1348
```

(2) INFORMATION FOR SEQ ID NO: 177:

  (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 1502 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: double
      (D) TOPOLOGY: linear

  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

```
CTCAAAATAA ATAAATAAAT AAAAATTTGT ATTCCATTGA TTTGGGTAGA CACCAGGAAT         60

GTGCATTTCT AACAAGCTTT CCAGGCGATC CTATAGTAAG TCATCTGTGG ACTACTTTAA        120

GAAACTCTTC TATAGAGAAT GGAGTTGGAT TAATAATAGG TGATTTTTTA CACTGGACTG        180

ATTCACAAGA ACCTAAACAG TAGTCCATGA AGCTGCTCAT CTGTGGTAAC TATTTGGCCC        240

CGTCTCACTC TGAAAGCAGC AGGAGATGTT GTTTACTTTG TTTCTATCCC CTTTGTCTGG        300

AGATTAATTT TGGAATGAAA GTTTTTCTCT CTATGCCATT CCTGGTTCTT TTCCAAAGCC        360

TCATACAAGA GGATTAGGTC ACAATGCATG CATTACCTTT TAAAGAATG CGATATTGAT         420

ACCGATGCTT ACTTTTTTTT TTTTTNACTA CTTGTTTTAT TCCTTCCAGN AAAGTATAGC        480

CCGCCTTTCT ATAGCATAGT TCTCTTTAGG TGGAATGATT CCTATAAGAT TTCTCATTAT        540

TAAATCATGC ATTTTTCAAG ATGGAATCAA TMTTTGATTT AATCTAAGCT GATATTCTCA        600

TTTGTTAGAA GAACAACCTA CATGCTAGAG AGAGAGGAGG AAATATACCC ACGACCACAC        660
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        AGCCAGTTAG TATCCAGTTG GTGCTGGACT CCAGCCAGGT GTCCTGCCTC ATGGTAGTTA      720

        AATGATATAT AGAAAAGGTA AATTTTTAAA GAAATATTTA TTAATATATT CCTATAAAAC      780

        ATTTTAAAGG TAACCACATA AAAATGGTTA ATTTTTCCAT TCCAAAGTAA ATGCTAAGCA      840

        TGTTTATTAA TGAAGCAGTA CTTCTGATTA GTATATGACA TTCTGAAGTT AATTAAACTC      900

        ATTGCACTAA ATGTGTCTTC CTTGGTATAG TGGAGGATTT GAGGATTGGA ATATAGAGTA      960

        GAGTGCTTGC TTAAGCCTGG GAGCCCATCT TTATAGCTAT TTGATGTAAG AAAAGAGACA     1020

        TGGNCCATTT CTAAACTATA TAAGGTGAGT GTGTCTATTC CCAGCAGATA TAAAGGAAAA     1080

        AGGAAACTTT TTTGATTCCC ACCTTCCCAG CCTCACCTAG CCATCTTCCA GCCTCAAATA     1140

        TAGAGATGTT AGTGCAAGGT CCTGGGCTCT AGGTGATCAT TTCATAAGTC CTTTACAGAT     1200

        AAAGAAAAAG TAGTGTTTGT ATGTTTGTTT TTAAGTAACC CCAAAACAAA TTTATATTGT     1260

        ATTCAGCAAA ATTGGAATTC AGGTGTTTAA TTTTAGAACA TGAAGTGCCT GCTGTTTTAA     1320

        GCATTGACTT GTATAAAAAG AATTGCATGT CTCCAGTAAG CTTATGGGTT TTCTCATTTT     1380

        TAGGTATATG GCTTTTAATC ATGTAAAGTG AAACATTAGT TTTCTTGCAT TTTATTACAG     1440

        GTTCTTTGTT GCAATAAAGA TGCTGCTGAA ATTAATTGAA AAAAAAAAA AAAAAAACTC      1500

        GA                                                                    1502
```

(2) INFORMATION FOR SEQ ID NO: 178:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1637 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

```
        ATTTTCTAGC CCACAAGGAC TGAAGTTCAG ATCCAAAAGT TCACTTGCTA ATTATCTTCA       60

        CAAAAATGGA GAGACTTCTC TTAAGCCAGA AGATTTTGAT TTTACTGTAC TTTCTAAAAG      120

        GGGTATCAAG TCAAGATATA AAGACTGCAG CATGGCAGCC CTGACATCCC ATCTACAAAA      180

        CCAAAGTAAC AATTCAAACT GGAACCTCAG GACCCGAAGC AAGTGCAAAA AGGATGTGTT      240

        TATGCCGCCA AGTAGTAGTT CAGAGTTGCA GGAGAGCAGA GGACTCTCTA ACTTTACTTC      300

        CACTCATTTG CTTTTGAAAG AAGATGAGGG TGTTGATGAT GTTAACTTCA GAAAGGTTAG      360

        AAAGCCCAAA GGAAAGGTGA CTATTTTGAA AGGAATCCCA ATTAAGAAAA CTAAAAAAGG      420

        ATGTAGGAAG AGCTGTTCAG GTTTTGTTCM AAGTGATAGC AAAAGAGAAT CTGTGTGTAA      480
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      TAAAGCAGAT GCTGAAAGTG AACCTGTTGC ACAAAAAAGT CAGCTTGATA GAACTGTCTG      540

      CATTTCTGAT GCTGGAGCAT GTGGTGAGAC CCTCAGTGTG ACCAGTGAAG AAAACAGCCT      600

5     TGTAAAAAAA AAAGAAAGAT CATTGAGTTC AGGATCAAAT TTTTGTTCTG AACAAAAAAC      660

      TTCTGGCATC ATAAACAAAT TTTGTTCAGC CAAAGACTCA GAACACAACG AGAAGTATGA      720

      GGATACCTTT TTAGAATCTG AAGAAATCGG AACAAAGTA GAAGTTGTGG AAAGGAAAGA       780

10    ACATTTGCAT ACTGACATTT TAAAACGTGG CTCTGAAATG GACAACAACT GCTCACCAAC      840

      CAGGAAAGAC TTCACTGAAG ATACCATCCC ACGGAACACA GATAGAAAGA AGGAAAACAA      900

15    GCCTGTATTT TTCCAGCAAA TATAACAAAG AAGCTCTTAG CCCCCCACGA CGTAAAGCCT      960

      TTAAGAAATG GACACCTCCT CGGTCACCTT TTAATCTCGT TCAAGAAACA CTTTTTCATG     1020

      ATCCATGGAA GCTTCTCATC GCTACTATAT TTCTCAATCG GACCTCAGGC AAAATGGCAA     1080

20    TACCTGTGCT TTGGAAGTTT CTGGAGAAGT ATCCTTCAGC TGAGGTAGCA AGAACCGCAG     1140

      ACTGGAGAGA TGTGTCAGAA CTTCTTAAAC CTCTTGGTCT CTACGATCTT CGGGCAAAAA     1200

25    CCATTGTCAA GTTCTCAGAT GAATACCTGA CAAAGCAGTG GAAGTATCCA ATTGAGCTTC     1260

      ATGGGATTGG TGCACCCTGA AGACCACAAA TTAAATAAAT ATCATGACTG GCTTTGGGAA     1320

      AATCATGAAA AATTAAGTCT ATCTTAAACT CTGCAGCTTT CAAGCTCATC TGTTATGCAT     1380

30    AGCTTTGCAC TTCAAAAAAG CTTAATTAAG TACAACCAAC CACCTTTCCA GCCATAGAGA     1440

      TTTTAATTAG CCCAACTAGA AGCCTAGTGT GTGTGCTTTC TTAATGTGTG TGCCAATGGT     1500

35    GGATCTTTGC TACTGAATGT GTTTGAACAT GTTTTGAGAT TTTTTTAAAA TAAATTATTA     1560

      TTTGACAACA ATCCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA     1620

      AAAAAAAAAA AAAAAAA                                                    1637
40
```

```
      (2) INFORMATION FOR SEQ ID NO: 179:
45
            (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 2911 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
50                (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

      GGTGGTTTTT GTTCTGCAAT AGGCGGCTTA GAGGGAGGGG CTTTTTCGCC TATACCTACT       60
55
      GTAGCTTCTC CACGTATGGA CCCTAAAGGC TACTGCTGCT ACTACGGGGC TAGACAGTTA      120

      CTGTCTCAGC TCTAGGATGT GCGTTCTTCC ACTAGAAGCT CTTCTGAGGG AGGTAATTAA      180

60    AAAACAGTGG AATGGAAAAA CAGTGCTGTA GTCATCCTGT AATATGCTCC TTGTCAACAA      240
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TGTATACATT CCTGCTAGGT GCCATATTCA TTGCTTTAAG CTCAAGTCGC ATCTTACTAG    300

TGAAGTATTC TGCCAATGAA GAAAACAAGT ATGATTATCT TCCAACTACT GTGAATGTGT    360

GCTCAGAACT GGTGAAGCTA GTTTTCTGTG TGCTTGTGTC ATTCTGTGTT ATAAAGAAAG    420

ATCATCAAAG TAGAAATTTG AAATATGCTT CCTGGAAGGA ATTCTCTGAT TTCATGAAGT    480

GGTCCATTCC TGCCTTTCTT TATTTCCTGG ATAACTTGAT TGTCTTCTAT GTCCTGTCCT    540

ATCTTCAACC AGCCATGGCT GTTATCTTCT CAAATTTTAG CATTATAACA ACAGCTCTTC    600

TATTCAGGAT AGTGCTGAAG ANGCGTCTAA ACTGGATCCA GTGGGCTTCC CTCCTGACTT    660

TATTTTTGTC TATTGTGGCC TTGACTGCCG GGACTAAAAC TTTACAGCAC AACTTGGCAG    720

GACGTGGATT TCATCACGAT GCCTTTTTCA GCCCTTCCAA TTCCTGCCTT CTTTTCAGAA    780

ATGAGTGTCC CAGAAAAGAC AATTGTACAG CAAAGGAATG GACTTTTCCT GAAGCTAAAT    840

GGAACACCAC AGCCAGAGTT TTCAGTCACA TCCGTCTTGG CATGGGCCAT GTTCTTATTA    900

TAGTCCAGTG TTTTATTTCT TCAATGGCTA ATATCTATAA TGAAAAGATA CTGAAGGAAG    960

GGAACCAGCT CACTGAARGC ATCTTCATAC AGAACAGCAA ACTCTATTTC TTTGGCATTC   1020

TGTTTAATGG GCTGACTCTG GGCCTTCAGA GGAGTAACCG TGATCAGATT AAGAACTGTG   1080

GATTTTTTTA TGGCCACAGT GCATTTTCAG TAGCCCTTAT TTTTGTAACT GCATTCCAGG   1140

GCCTTTCAGT GGCTTTCATT CTGAAGTTCC TGGATAACAT GTTCCATGTC TTGATGGCCC   1200

AGGTTACCAC TGTCATTATC ACAACAGTGT CTGTCCTGGT CTTTGACTTC AGGCCCTCCC   1260

TGGAATTTTT CTTGGAAGCC CCATCAGTCC TTCTCTCTAT ATTTATTTAT AATGCCAGCA   1320

AGCCTCAAGT TCCGGAATAC GCACCTAGGC AAGAAAGGAT CCGAGATCTA AGTGGCAATC   1380

TTTGGGAGCG TTCCAGTGGG GATGGAGAAG AACTAGAAAG ACTTACCAAA CCCAAGAGTG   1440

ATGAGTCAGA TGAAGATACT TTCTAACTGG TACCCACATA GTTTGCAGCT CTCTTGAACC   1500

TTATTTTCAC ATTTTCAGTG TTTGTAATAT TTATCTTTTC ACTTTGATAA ACCAGAAATG   1560

TTTCTAAATC CTAATATTCT TTGCATATAT CTAGCTACTC CCTAAATGGT TCCATCCAAG   1620

GCTTAGAGTA CCCAAAGGCT AAGAAATTCT AAAGAACTGA TACAGGAGTA ACAATATGAA   1680

GAATTCATTA ATATCTCAGT ACTTGATAAA TCAGAAAGTT ATATGTGCAG ATTATTTTCC   1740

TTGGCCTTCA AGCTTCCAAA AAACTTGTAA TAATCATGTT AGCTATAGCT TGTATATACA   1800

CATAGAGATC AATTTGCCAA ATATTCACAA TCATGTAGTT CTAGTTTACA TGCCAAAGTC   1860

TTCCCTTTTT AACATTATAA AAGCTAGGTT GTCTCTTGAA TTTTGAGGCC CTAGAGATAG   1920

TCATTTTGCA AGTAAAGAGC AACGGGACCC TTTCTAAAAA CGTTGGTTGA AGGACCTAAA   1980

TACCTGGCCA TACCATAGAT TTGGGATGAT GTAGTCTGTG CTAAATATTT TGCTGAAGAA   2040
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GCAGTTTCTC AGACACAACA TCTCAGAATT TTAATTTTTA GAAATTCATG GGAAATTGGA   2100

TTTTTGTAAT AATCTTTTGA TGTTTTAAAC ATTGGTTCCC TAGTCACCAT AGTTACCACT   2160

TGTATTTTAA GTCATTTAAA CAAGCCACGG TGGGGCTTTT TTCTCCTCAG TTTGAGGAGA   2220

AAAATCTTGA TGTCATTACT CCTGAATTAT TACATTTTGG AGAATAAGAG GGCATTTTAT   2280

TTTATTAGTT ACTAATTCAA GCTGTGACTA TTGTATATCT TTCCAAGAGT TGAAATGCTG   2340

GCTTCAGAAT CATACCAGAT TGTCAGTGAA GCTGATGCCT AGGAACTTTT AAAGGGATCC   2400

TTTCAAAAGG ATCACTTAGC AAACACATGT TGACTTTTAA CTGATGTATG AATATTAATA   2460

CTCTAAAAAT AGAAAGACCA GTAATATATA AGTCACTTTA CAGTGCTACT TCACACTTAA   2520

AAGTGCATGG TATTTTTCAT GGTATTTTGC ATGCAGCCAG TTAACTCTCG TAGATAGAGA   2580

AGTCAGGTGA TAGATGATAT TAAAAATTAG CAAACAAAAG TGACTTGCTC AGGGTCATGC   2640

AGCTGGGTGA TGATAGAAGA GTGGGCTTTA ACTGGCAGGC CTGTATGTTT ACAGACTACC   2700

ATACTGTAAA TATGAGCTTT ATGGTGTCAT TCTCAGAAAC TTATACATTT CTGCTCTCCT   2760

TTCTCCTAAG TTTCATGCAG ATGAATATAA GGTAATATAC TATTATATAA TTCATTTGTG   2820

ATATCCACAA TAATATGACT GGCAAGAATT GGTGGAAATT TGTAATTAAA ATAATTATTA   2880

AACCTAAAAA AAAAAAAAAA AAAAACTCGA G   2911

(2) INFORMATION FOR SEQ ID NO: 180:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 519 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GGCACGAGCC CCAGGCCAGC CAGGGCCAGG CCTACTTTGG CCACCCTTAA ATTAGAATGT   60

GGGGTCAGGG GTCACAGAAA AGCCATTTCT CTGACCTAGT GTTTGGCGTC CGGGAACTCT   120

GTGCCCAACC TTCAGACCCT GGCAGTCCTC ACTGAGGCCA TTGGCCCAGA GCCCGCCATC   180

CCCCGARACC CCCGGGAGCC GCCTGTTGCC ACGTCCACAC CTGCCACACC CTCTGCCGGG   240

CCCCAGCCCC TCCCAACCGG GACCGTGCTG GTCCCTGGGG TCCTGCCCC ACCTTGCCTT   300

GGGGAGGCAT GGGCCCTCCT CCTCCCACCC TGCCGGCCGT CACTCACCTC TTGCTTCTGG   360

TCCCCCAGGC CTAGCCCTTG GAAGGAGACA GGAGTCTAGG GAGGCTGAAG CCCACTCCCG   420

GGGAGGCCCG TGCTCCTCCA GCCCCAGGGA CAGCAAGGAA AAGAGAAGAG AGCAGAGCAT   480

433

TTCATGGCTC TAATAAAAAA AAAAAAAAAA AAAACTCGA   519

5

(2) INFORMATION FOR SEQ ID NO: 181:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 968 base pairs
10   (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:
15

TCCCCTTGGG GCCGGAAAAA GCGGGGTTGG CCTGNCCATT GGTTNTCCAT GCCGCCCGCC   60

CATGCCCCAG TACTAGCCTG CAGTCCCAAT GTAGCCCCTC CCTCYTCCMA GAGCCCYTCM   120

20 AACCGCCCCG STCANTTGTG ATTTCAGGAG GATTTGATGA AGATGTTAAA GCGAAAGTGG   180

AGAACCTTCT CGGGATTTCC AGCCTGGAAA AAACGGACCC TGTTAGGCAA GCACCCTGCA   240

GCCCTCCCTG TCCCCTTCTT CCCCTCCCCT TCYCCCGCCC GTGGAGACAG CTGTTYTCAG   300

25 CAGGGCTCTC CGCAGGGAGG GGGCCGGCTC CTTCCCTGGC AGCAACATCC TTGCCCTTGT   360

CACACAAGTC AGCCTCCATC TGCGCAGCTC TGTGGATGCG CTGCTGGAGG GCAACAGGTA   420

30 TGTCACTGGC TGGTTCAGCC CCTACCACCG CCAGCGGAAG CTCATCCACC CGGTCATGGT   480

TCAGCACATC CAGCCCGCAG CGCTCAGCCT CCTGGCACAG TGGAGCACCC TCGTGCAGGA   540

GCTGGAGGCT GCCCTGCAGC TGGCTTTCTA CCCGGATGCC GTGGAGGAGT GGCTGGAGGA   600

35 AAACGTGCAC CCCAGCCTGC AGCGGCTGCA ARCTCTGCTG CAGGACCTCA GCGAGGTGTC   660

TGCCCCCCCG CTGCCACCCA CCAGCCCTGG CAGGGACGTT GCTCAGGACC CCTGAGGGGA   720

GAGCTCATGC CAGGGGGCTC CTGCTGGAGG CTGGGGGGGC TCTGCWYTKY CWWWTGGCCT   780

40 GGGCAATACG GCCCACGTGG GCGTCGTGCC CTCTGGCCCA GCAGTGTCTT GCCCACACTC   840

AGTTCCTGAG GGCCCTGGGC AGCCCCTGGG GGAGAGACTA GAAAACACAG AAGGAAGCAG   900

45 CACAGGGAGA CCCGCTTTGT GATCTGCATG TGTGACACTG ATTCTTTGGA AATAAAGAGT   960

GGAAGCTG   968

50

(2) INFORMATION FOR SEQ ID NO: 182:

55   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1128 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear
60

434

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

```
TGTAAAAGTT ATCAGTAATC CTAATTCTTT TCCTGGGTTT TCCTTTTGTC ACTTATTAAT        60

5    CAGTTTTTGA AAGGACGAAT GAATTTAGAG ATGTACTCTG GAGCAGTATC ATGTTAAACC        120

     AGGGGTATAT TAGAAAAATC ATCCTCATAA TCATTCTGGG AAGTTTTTCC TCCCCAAAAA        180

     AAGCCATCCT GATGGGTTTT CAAAACCAGA AAAAAGCTCT TAATGAGGAA CAGACCACTG        240

10   GAGTACCCAT GAGCATCTCA GGAAAACTGA GACCCTCGAG AAGCCTTGAT TTCGTGCAAC        300

     CCCCAAGGTT TCAGAGCCAG CAGCCCAGTG CTGTGGTTGA CAGACGTGGT TTTKTGGRGA        360

15   AAGCAGCCAG AGGCCAGGAA TTTTCAGAGT CGTGAGTCAC GRTYTCCCAC CCAAGATTAG        420

     AGCAMAGATT AGCCATACTG AGATTTGGTA AAATCATTCT GTCTAAGCAA TGGAGGTGTG        480

20   TGCAMACGTG CAGTGCCTGT TCACAGGGGA TGCAGGCAGA TCSYGGGTTT AGGATGGGGR        540

     AGGCCACCGC ACCCCCYTTC AYTGCTCTGC ACCTGCTCCC TCACGTGGAC ACTGTCCACA        600

     ACTGTGGCTC TCACAGGACA GTTGCCCAAG GAGCTCATAT CTTATTGGAG ATAGGGGGTC        660

25   GTACAGGTGA CATTCATGAG CAGTGTGAGC CGGGTGACAT GGGGGTGTCA ACCCAGCATC        720

     TGTCCAGGAG CTCCTCCTGC AGCGGCTCTG GCAGGTGGCC TGAGGCTCCT TTTTGAGAGA        780

     GAACTGTTTG GCCTTCCTGT CTCCTCTCCT CTGATCTGTT CTTTCTTGGA ACACCACCCA        840

30   AGAACGTCAC CTCCTCCATC AGATTGTGAG CTCCTGGAGG GCAGGAGCTG TGTCCTTCTA        900

     TTCATCTTCC TATCCCCAGA ACCTTGCACA GATCCTGGAA TGTGGTAGGT GCTCAGTAAA        960

35   TGTGTGTTGA ATAAATGAAT GAATGAATGA ACAAATGAAT GAATTTGCTT ACTTCAAGGC        1020

     AAAAGAACCA TGAAACTGTA TTTRGAGTTT CTATGTTATA GCAGTCAGCA AATCCTATTA        1080

     AATACTTTGT GTTTCCAAGC AAAAAAAAAA AAAAAAAAAA AAACTCGA        1128

40
```

45   (2) INFORMATION FOR SEQ ID NO: 183:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2276 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
50   (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

```
CCGCGGCGTC TGACCTCATG GCGTAGAGCC TAGCAACAGC GCAGGCTCCC AGCCGAGTCC        60

55   GTTATGGCCG CTGCCGTCCC GAAGAGGATG AGGGGGCCAG CACAAGCGAA ACTGCTGCCC        120

     GGGTCGGCCA TCCAAGCCCT TGTGGGGTTG GCGCGGCCGC TGGTCTTGGC GCTCCTGCTT        180

60   GTGTCCGCCG CTCTATCCAG TGTTGTATCA CGGACTGATT CACCGAGCCC AACCGTACTC        240
```

```
        AACTCACATA TTTCTACCCC AAATGTGAAT GCTTTAACAC ATGAAAACCA AACCAAACCT        300

        TCTATTTCCC AAATCAGCAC CACCCTCCCT CCCACGACGA GTACCAAGAA AAGTGGAGGA        360
    5
        GCATCTGTGG TCCCTCATCC CTCGCCTACT CCTCTGTCTC AAGAGGAAGC TGATAACAAT        420

        GAAGATCCTA GTATAGAGGA GGAGGATCTT CTCATGCTGA ACAGTTCTCC ATCCACAGCC        480

   10   AAAGACACTC TAGACAATGG CGATTATGGA GAACCAGACT ATGACTGGAC CACGGGCCCC        540

        AGGGACGACG ACGAGTCTGA TGACACCTTG GAAGAAAACA GGGGTTACAT GGAAATTGAA        600

        CAGTCAGTGA AATCTTTTAA GATGCCATCC TCAAATATAG AAGAGGAAGA CAGCCATTTC        660
   15
        TTTTTTCATC TTATTATTTT TGCTTTTTGC ATTGCTGTTG TTTACATTAC ATATCACAAC        720

        AAAAGGAAGA TTTTTCTTCT GGTTCAAAGC AGGAAATGGC GTGATGGCCT TTGTTCCAAA        780

   20   ACAGTGGAAT ACCATCGCCT AGATCAGAAT GTTAATGAGG CAATGCCTTC TTTGAAGATT        840

        ACCAATGATT ATATTTTTTA AAGCACTGTG ATTTGAATTT GCTTATGTAA TTTTATTTGC        900

        TTGACTTTTT ATATGATATT GTGCAAATGT TTGCCATAGG CAATTGGTAC TTAAATGAGA        960
   25
        GGTGAGTCTC TCTTTTGCCT TGGTGCTTTG GAAATTAAAT GTCACAAACG AGTATATAAT       1020

        TTTTTATCTG TACTTTTAGA GCTGAGTTTA ATCAGGTGTC CAAAATGTGA GTTAAACATT       1080

   30   ACCTTATATT TACACTGTTA GTTTTTATTG TTTTAGATTT ATTATGCTTC TTCTGGAAGT       1140

        ATTAGTGATG CTACTTTTAA AAGATCCCAA ACTTGTAACT AAATTCTGAC ATATCTGTTA       1200

        CTGCTGACTC ACATTCATTC TCCGCCATTC AAATACTATT TTTTATCCAC ATTTTTTTTT       1260
   35
        GTTCCCAAAC TGTAATGTAC AAGGATATGT GTGATAATGC TTTGGATTTG AGTAATATTT       1320

        TTTTTTCTTC CAAGAAAACT GCTTTGGATA TTTTTAGATA ATTTAAACAT AATTTAGGAT       1380

   40   AATGATATTG CTCAATCTGA CCACAATTTT AGGTAAAACA TTAAATGTGT CAGAAATCTT       1440

        GGCAACAGAG ACTCTGCAGC TTGCAGTGGA CATAGATAAA ATGTTACAGA GATACTATTT       1500

        TTTTGGTTGG AATTACTATA TTAAATTTAG AAGCAGAAAC TGGTAAAATG TTAAATACAT       1560
   45
        GTACAATTGC TTTTAGTTAG CAATTGATTG TAGCATGGGT TCCTCCAAGG TTTCAAGCAA       1620

        TGGGCAGAGT TTAAAATTAT ATCAGATTCG TTTACTTCGT TTATTATTTT ACAGTAAATT       1680

   50   TGAATAAATC TTAGGGGTCA TTATCACTTA AATAATACTG TACCTAGGTC TTTCAAATTA       1740

        AAATTATACC TGAATGAAGT TGTTTGTATA CATAAAGGAT ATTTGTGTAC AATTACCTTT       1800

        TTTCCCCCAC ACTTGTTTTC TTTGTTTTTG TTTTTTATGG CAACTGGAAA GTATTTACTA       1860
   55
        TGGGATTCAT TTATGTCTGT CTTTCTATCA TAAAGAATTG ATCAATATGT AAATATGTGA       1920

        TTTGAACCAT GGTTGACTTA CAAGTGTCAC TACAGCTTTT TAGAAAACAT AGCCCTAATA       1980

   60   TATGTTAAGC AGGACCCGGG TGAGCCAGTG GGCTTGCGCT TTATGTAGAG CTGGAAGAAG       2040
```

436

```
GCCGTCCATC CTGTCTCTTG GGCGGACAGT GTACTTTCCT AATAGGGAAG GGAAGCACAA        2100

TGGAAATACC CCTGAACCGT TTTATTGCAG TAATTTTTTT CATATCTGAA ACTATTATTT        2160

AATATTTTGA ATAAGATTTT AAAAAATAAA TGGCAAAGAT ATAAATCTAA AAAAAAAAAA        2220

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAA          2276
```

(2) INFORMATION FOR SEQ ID NO: 184:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 2500 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

```
TCCAAGCTAC GCCACTCGGG CTGGGGCGTT GGGAGCGGGA GTGCAGAGCG TGGTCGTGGC         60

GGCGGCGGTG AGAAGAGCGA GGCGKAGGAG GGGGTGCCAT GGCCGGGCAG CAGTTCCAGT        120

ACGATGACAG TGGGAACACC TTCTTCTACT CCTCACCTC CTTCGTGGGG CTCATCGTGA        180

TCCCGGCGAC ATACTACCTC TGGCCCCGAG ATCAGAATGC CGAGCAAATT CGATTAAAGA        240

ATATCAGAAA AGTATATGGA AGGTGTATGT GGTACGTTTA CGGTTATTAA AACCCCAGCC        300

AAATATTATT CCTACAGTAA AGAAAATAGT TCTGCTTGCA GGATGGGCAT TGTTCTTATT        360

CCTTGCATAT AAAGTTTCCA AAACAGACCG AGAATACCAA GAATACAATC CTTATGAAGT        420

ATTAAATTTG GATCCTGGAG CCACAGTAGC AGAAATTAAA AAACAATATC GTTTGCTGTC        480

ACTTAAATAT CATCCAGATA AAGGAGGTGA TGAGGTTATG TTCATGAGGA TAGCAAAAGC        540

TTATGCTGCT TTAACGGATG AAGAGTCCCG GAAAAATTGG GAAGAATTTG AAATCCAGA        600

TGGGCCTCAA GCCACAAGCT TTGGAATTGC CCTGCCAGCT TGGATAGTTG ACCAGAAAAA        660

TTCAATTCTG GTTTTACTTG TATATGGATT GGCATTTATG GTTATCCTTC CAGTTGTTGT        720

GGGCTCTTGG TGGTATCGCT CAATACGCTA TAGTGGAGAC CAGATTCTAA TACGSACAAC        780

ACAGATTTAT ACATACTTTG TTTATAAAAC CCGAAATATG GATATGAAAC GTCTTATCAT        840

GGTTTTGGST GGAGCTTCTG AATTTGATCC TCAGTATAAT AAAGATGCCA CAAGCAGACC        900

AACGGATAAT ATTCTAATAC CACAGCTAAT CAGAGAAATT GGCAGCATTA ATTTAAAGAA        960

GAATGAGCCT CCACTTACCT GCCCATATAG CCTGAAGGCC AGAGTTCTTT TACTGTCTCA       1020

TCTTGCTAGA ATGAAAATTC CTGAGACCCT TGAAGAAGAT CAGCAATTCA TGCTAAAAAA       1080

GTGTCCTGCC CTACTTCAAG AAATGGTTAA TGTAATCTGC CAACTAATAG TAATGGCCCG       1140
```

```
GAACCGTGAA GAAAGGGAGT TTCGTGCTCC AACTTTGGCA TCCCTAGAAA ACTGCATGAA        1200

GCTTTCTCAG ATGGCCGTTC AGGGACTTCA GCAATTTAAG TCTCCCCTTC TGCAGCTCCC        1260

TCATATTGAA GAGGACAATC TTAGACGGGT TTCTAATCAT AAGAAGTATA AAATTAAAAC        1320

TATCCAGGAT TTGGTGAGTT TAAAAGAATC AGATCGTCAC ACTCTACTGC ACTTCCTTGA        1380

AGATGAAAAA TATGAAGAGG TTATGGCTGT CCTTGGGAGT TTTCCATATG TGACCATGGA       . 1440

TATAAAATCA CAGGTGTTAG ATGATGAAGA TAGCAACAAC ATCACAGTAG GATCCTTAGT        1500

TACAGTGTTG GTTAAGTTGA CAAGGCAAAC AATGGCTGAA GTATTTGAAA AGGAGCAGTC        1560

CATCTGTGCT GCAGAGGAAC AGCCAGCAGA AGATGGGCAG GGTGAAACTA ACAAGAACAG        1620

GACAAAAGGA GGATGGCAAC AGAAGAGTAA AGGACCCAAG AAAACTGCTA AATCAAAAAA        1680

AAAGAAACCT TTAAAAAAAA AACCTACACC TGTGCTATTA CCACAGTCAA AGCAACAGAA        1740

ACAAAAGCAG GCAAATGGAG TCGTTGGGAA TGAAGCTGCA GTAAAGGAAG ATGAAGAAGA        1800

AGTTTCAGAT AAGGGCAGTG ATTCTGAAGA AGAAGAAACC AATAGAGATT CCCAAAGTGA        1860

GAAAGATGAT GGTAGTGACA GAGACTCTGA TAGAGAGCAA GATGAAAAAC AAAACAAAGA        1920

TGATGAAGCA GAGTGGCAAG AATTACAACA AAGCATACAG CGAAAAGAGA GAGCTCTATT        1980

GGAAACCAAA TCAAAAATAA CACATCCTGT GTATAGCCTT TACTTTCCTG AGGAAAAACA        2040

AGAATGGTGG TGGCTTTACA TTGCAGATAG GAAGGAGCAG ACATTAATAT CCATGCCATA        2100

TCATGTGTGT ACGCTGAAAG ATACAGAGGA GGTAGAGCTG AAGTTTCCTG CACCAGGCAA        2160

GCCTGGAAAT TATCAGTATA CTGTGTTTCT GAGATCAGAC TCCTATATGG GTTTGGATCA        2220

GATTAAACCA TTGGAAGTTK GGAAGTTCAT GAGGCTGAAG CCTGTGCCAG AAAATCACCC        2280

ACAGTGGGAT ACAGCAATAG AGGGGGATGA AGACCAGGAG GACAGTGAGG GCTTTGAAGA        2340

TAGCTTTGAG GGAGGAAGAG GGAGGGAGGA AGGAAGGTGG TGGACTTAAG GCAGTTACTC        2400

TGGAATGGGA CCCACAGTGT TTTGCACCAT ATTTTGGCAA TTTTTTTTGC CCGTTTTTNG        2460

GAAGTGTTTT CCNTNAANCC CAGGAACCAT TACAGAACCG                              2500
```

(2) INFORMATION FOR SEQ ID NO: 185:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1337 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

```
CTTCCGGTTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC              60
```

438

```
TCTCCCTGGC GTTTGGTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA        120

GCCAGCGTGG CGGGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG        180

GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCTCCT CCTGCTGTTG        240

CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT        300

CTTGGGCCTC CTGACCCTAG ACCACGGACA TTACCGCCGC TGCCACCGGG CCCTACCCCT        360

GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGGC CGCGGGGCTC CGAGGGAGGC        420

AATGGCAGCA ACCCTGTGGC CGGGCTTGAG ACGGACGATC ACGGAGGGAA GGCCGGGGAA        480

GGCTCGGTGG GTGGCGGCCT TGCTGTGAGC CCCAACCCTG GCGACAAGCC CATGACCCAG        540

CGGGCCCTGA CCGTGTTGAT GGTGGTGAGC GGCGCGGTGC TGGTGTACTT CGTGGTCAGG        600

ACGGTCAGGA TGAGAAGAAG AAACCGAAAG ACTAGGAGAT ATGGAGTTTT GGACACTAAC        660

ATAGAAAATA TGGAATTGAC ACCTTTAGAA CAGGATGATG AGGATGATGA CAACACGTTG        720

TTTGATGCCA ATCATCCTCG AAGATAAGAA TGTGCCTTTT GATGAAAGAA CTTTATCTTT        780

CTACAATGAA GAGTGGAATT TCTATGTTTA AGGAATAAGA AGCCACTATA TCAATGTTGG        840

GGGGGTATTT AAGTTACATA TATTTTAACA ACCTTTAATT TGCTGTTGCA ATAAATACCG        900

TATCCTTTTA TTATATCTTT ATATGTATAG AAGTACTCTR TTAATGGGCT CAGAGATGTT        960

GGGGATAAAG TATACTGTAA TAATTTATCT GTTTGAAAAT TACTATAAAA CGGTGTTTTC       1020

TGATCGGTTT TTGTTTCCTG CTTACCATAT GATTGTAAAT TGTTTTATGT ATTAATCAGT       1080

TAATGCTAAT TATTTTTGCT GATGTCATAT GTTAAAGAGC TATAAATTCC AACAACCAAC       1140

TGGTGTGTAA AAATAATTTA AAATTTCCTT TACTGAAAGG TATTTCCCAT TTTTGTGGGG       1200

AAAAGAAGCC AAATTTATTA CTTTGTGTTG GGGTTTTTAA AATATTAAGA AATGTCTAAG       1260

TTATTGTTTG CAAAACAATA AATATGATTT TAAATTCTCT TAAAAAAAAA AAAAAAAACC       1320

CCGGGGGGGG GCCCGGN                                                      1337
```

(2) INFORMATION FOR SEQ ID NO: 186:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 941 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

```
GGCACGAGCC TGGACGCAGC AGCCACCGCC GCGTCCCTCT CTCCACGAGG CTGCCGGCTT         60
```

```
AGGACCCCCA GCTCCGACAT GTCGCCCTCT GGTCGCCTGT GTCTTCTCAC CATCGTTGGC      120

CTGATTCTCC CCACCAGAGG ACAGACGTTG AAAGATACCA CGTCCAGTTC TTCAGCAGAC      180

TCAACTATCA TGGACATTCA GGTCCCGACA CGAGCCCCAG ATGCAGTCTA CACAGAACTC      240

CAGCCCACCT CTCCAACCCC AACCTGGCCT GCTGATGAAA CACCACAACC CCAGACCCAG      300

ACCCAGCAAC TGGAAGGAAC GGATGGGCCT CTAGTGACAG ATCCAGAGAC ACACAAGAGC      360

ACCAAAGCAG CTCATCCCAC TGATGACACC ACGACGCTCT CTGAGAGACC ATCCCCAAGC      420

ACAGACGTCC AGACAGACCC CCAGACCCTC AAGCCATCTG GTTTTCATGA GGATGACCCC      480

TTCTTCTATG ATGAACACAC CCTCCGGAAA CGGGGGCTGT TGGTCGCAGC TGTGCTGTTC      540

ATCACAGGCA TCATCATCCT CACCAGTGGC AAGTGCAGGC AGCTGTCCCG GTTATGCCGG      600

AATCATTGCA GGTGAGTCCA TCAGAAACAG GAGCTGACAA CCYGCTGGGC ACCCGAAGAC      660

CAAGCCCCCT GCCAGCTCAC CGTGCCCAGC CTCCTGCATC CCCTCGAAGA GCCTGGCCAG      720

AGAGGGAAGA CACAGATGAT GAAGCTGGAG CCAGGGCTGC CGGTCCGAGT CTCCTACCTC      780

CCCCAACCCT GCCCGCCCCT GAAGGCTACC TGGCGCCTTG GGGGCTGTCC CTCAAGTTAT      840

CTCCTCTGYT AAGACAAAAA GTAAAGCACT GTGGTCTTTG CAAAAAAAAA AAAAAAAAAA      900

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAACTCG A                         941
```

(2) INFORMATION FOR SEQ ID NO: 187:

          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 654 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

```
GAATTCGGCA CGAGGCAGCT TGTGCTTTAA AGGAGGTGTT CAAAGCATGT CTGAGCAGAG       60

ACTTTTGGGC TCTGTTTTAA TTAATACTTT AAAATAATTC ATATTTAAAA TATCARATGT      120

TTCCATAAAG AGGAGGATGT TTAAATGCCT CCAGACTACA TTCCTTTTTA TTSCTTGATT      180

TTACCTGGGA GTCCAAAGTT CAATTCCCAT AAAGCAAGCG TTTTATTTGT CACTTTCAAT      240

ATACATCCGA TTGCCATGCT TAAGATGCAA TATGGGCTGC GGAAATAGGT TAACCCACAG      300

GCTCCCAGGG CCCAGTGTAG AAGGTGAGAG ATTCGTGTAA AATGATTCAA ATAAAAGGAA      360

GACCCTGGCC GGGTGCCGTA RCTCACGCCT GTAATCCCAG CACTTTGGGA GGCCGAAGCG      420

AGTGGATGAC GAGGTTAGGA GTTGGAGACC AGCCTGGCCA ACATCGTGAA ACCCCGTCTC      480

TACTAAAAAT ACAAAAATTA GCCGGGCATG GTGGCAGGCA CCTGTAATCC TAGCTAGTTG      540
```

440

```
GGAGGCTGAG GCAGGAGAAT CGTTTGAATC TGGGAGTTGG AGGTTGTCAG TGAGCTGAGA        600

TCGCGCCACA GCACTCCAGC CTGGGTGACA GGGTGAGACT CTGTCTCAAA NAGA             654
```

(2) INFORMATION FOR SEQ ID NO: 188:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1848 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

```
GAAACTGGAC CGGAGAACCG GAGCGAAGCG AAGCGGAAGC CCGGAATGAG GCCGGACTGG        60

AAAGCCGGAG CGGGGCCAGG CGGGCCTCCC CAAAAGCCTG CCCCTTCATC CCAGCGGAAA       120

CCGCCGGCCC GGCCGAGCGC GGCGGCCGCT GCGATTGCAG TCGCGGCGGC GGAGGAAGAG       180

AGACGGCTCC GGCAGCGGAA CCGCCTGAGG CTGGAGGAGG ACAAACCGGC CGTGGAGCGG       240

TGCTTGGAGG AGCTGGTCTT CGGCGACGTC GAGAACGACG AGGACGCGTT GCTGCGGCGT       300

CTGCGAGGCC CGAGGGTTCA AGAACATGAA GACTCGGGTG ACTCAGAAGT GGAGAATGAA       360

GCAAAAGGTA ATTTTCCACC TCAAAAGAAG CCAGTTTGGG TGGATGAAGA AGATGAAGAT       420

GAGGAAATGG TTGACATGAT GAACAATCGG TTTCGGAAGG ATATGATGAA AAATGCTAGT       480

GAAAGTAAAC TTTCGAAAGA CAACCTTAAA AAGAGACTTA AGAAGAATT CCAACATGCC        540

ATGGGAGGAG TACCTGCCTG GGCAGAGACT ACTAAGCGGA AAACATCTTC AGATGATGAA       600

AGTGAAGAGG ATGAAGATGA TTTGTTGCAA AGGACTGGGA ATTTCATATC CACATCAACT       660

TCTCTTCCAA GAGGCATCTT GAAGATGAAG AACTGCCAGC ATGCGAATGC TGAACGTCCT       720

ACTGTTGCTC GGATCTCCAT CTGTGCAGTT CCATCCCGGT GCACAGATTG TGATGGTTGC       780

TGGGATTAGA TAATGCTGTA TCACTATTTC AGGTTGATGG GAAAACAAAT CCTAAAATTC       840

AGAGCATCTA TTTGGAAAGG TTTCCAATCT TTAAGGCTTG TTTTAGTGCT AATGGGGAAG       900

AAGTTTTAGC CACGAGTACC CACAGCAAGG TTCTTTATGT CTATGACATG CTGGCTGGAA       960

AGTTAATTCC TGTGCATCAA GTGAGAGGTT TGAAAGAGAA GATAGTGAGG AGCTTTGAAG      1020

TCTCCCCAGA TGGGTCCTTC TTGCTCATAA ATGGCATTGC TGGATATTTG CATTTGCTAG      1080

CAATGAAGAC CAAAGAACTG ATTGGAAGCA TGAAAATTAA TGGAAGGGTT GCAGCATCCA      1140

CATTCTCTTC AGATAGTAAG AAAGTATACG CCTCTTCGGG GGATGGAGAA GTTTATGTTT      1200

GGGATGTGAA CTCAAGGAAG TGCCTTAACA GATTTGTTGA TGAAGGCAGT TTATATGGAT      1260
```

```
TAAGCATTGC CACATCTAGG AATGGACAGT ATGTTGCTTG TGGTTCTAAT TGTGGAGTGG    1320

TAAATATATA CAATCAAGAT TCTTGTCTCC AAGAAACAAA CCCAAAGCCA ATAAAAGCTA    1380

TAATGAACTT GGTTACAGGT GTTACTTCTC TGACCTTCAA TCCTACTACA GAAATCTTGG    1440

CAATTGCTTC AGAAAAAATG AAAGAAGCAG TCAGATTGGT TCATCTTCCT TCCTGTACAG    1500

TATTTTCAAA CTTCCCAGTC ATTAAAAATA AGAATATTTC TCATGTTCAT ACCATGGATT    1560

TTTCTCCGAG AAGTGGATAC TTTGCCTTGG GGAATGAAAA GGGCAAGGCC CTGATGTATA    1620

GGTTGCACCA TTACTCAGAC TTCTAAAGAG ACTATTTGAA GTCCAGTTGA GTCACAAGAG    1680

AAGCCTGTCT TGATATATCA TCTCAGAAAC TTTCCTGAAT ATGTGATAAT ATATGGAAAA    1740

TGATTTATAG ATCCAGCTGT GCTTAAGAGC CAGTAATGTC TTAATAAACA TGTGGCAGCT    1800

TTTGTTTGAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACTCGA              1848
```

(2) INFORMATION FOR SEQ ID NO: 189:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1146 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

```
AAAAAAAACC CAGGGGAACN TTGGGGGCCG CTTTNNNTTC CCCCTCCAGG CCATTGGGGA     60

ATTCTTCAAG TTAATCCTGC TTTGCTCTTG GCCAACAGGG CTTGTAGGGG GGAGAGACCC    120

AGGATCATCA AGGGGTTCGA GTGCAAGCCT CACTCCCAGC CCTGGCAGGC AGCCCTGTTC    180

GAGAAGACGC GGCTACTCTG TGGGGCGACG CTCATCGCCC CCAGATGGCT CCTGACAGCA    240

GCCCACTGCC TCAAGCCCCG CTACATAGTT CACCTGGGGC AGCACAACCT CCAGAAGGAG    300

GAGGGCTGTG AGCAGACCCG GACAGCCACT GAGTCCTTCC CCCACCCCGG CTTCAACAAC    360

AGCCTCCCCA ACAAAGACCA CCGCAATGAC ATCATGCTGG TGAAGATGGC ATCGCCAGTC    420

TCCATCACCT GGGCTGTGCG ACCCCTCACC CTCTCCTCAC GCTGTGTCAC TGCTGGCACC    480

AGCTGYCTCA TTTCCGGCTG GGGCAGMACG TCCAGCCCCC AGTTACGCCT GCCTCACACC    540

TTGSGATGCG CCAACATCAC CATCATTGAG CACCAGAAGT GTGAGAACGC CTACCCCGGC    600

AACATCACAG ACACCATGGT GTGTGCCAGC GTGCAGGAAG GGGGCAAGGA CTCCTGCCAG    660

GGTGACTCCG GGGGCCCTCT GGTCTGTAAC CAGTCTCTTC AAGGCATTAT CTCCTGGGGC    720

CAGGATCCGT GTGCGATCAC CCGAAAGCCT GGTGTCTACA CGAAAGTCTG CAAATATGTG    780

GACTGGATCC AGGAGACGAT GAAGAACAAT TAGACTGGAC CCACCCACCA CAGCCCATCA    840
```

```
CCCTCCATTT CCACTTGGTG TTTGGTTCCT GTTCACTCTG TTAATAAGAA ACCCTAAGCC      900

AAGACCCTCT ACGAACATTC TTTGGGCCTC CTGGACTACA GGAGATGCTG TCACTTAATA      960

ATCAACCTGG GGTTCGAAAT CAGTGAGACC TGGATTCAAA TTCTGCCTTG AAATATTGTG     1020

ACTCTGGGAA TGACAACACC TGGTTTGTTC TCTGTTGTAT CCCCAGCCCC AAAGACAGCT     1080

CCTGGCCATA TATCAAGGTT TCAATAAATA TTTGCTAAAT GAAAAARAAA AAAAAAAAAA     1140

ACTCGA                                                               1146
```

(2) INFORMATION FOR SEQ ID NO: 190:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 906 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

```
ACTCCCTCAC CCAGGTCCCA GCCCTGGGAA CCACCTACCG TGAGCCCTTT TGCAGATATA       60

GACTCATTTC ATCCTCAGAT GGTCCTTCAA GGTAGGTACT TTAGTCCCAT TTTAGAGATG      120

AGACGATTGA GGCCAGAGGG GTGNNGTAAC TTGCCTGGGG GCTCACGAGC ACAAAAGGAG      180

CCGAGGCAGG ATCTGACCCT TGTTCTCTGG CCTCACTGCC CTCACTTTGC CATGACCCGA      240

AGTTATGTCC CTACAAAGCA ATGCATGGTC CAAGGYTCTT TTTATTGTAT TTTTATTTTT      300

AAGGGTCCTG TTCAAAACTG GTGTGAGCTC TGAGGAGTCC TGAACCCTGG GTGCAGCATC      360

CTAGCATCCT GGGAGTCCTT TTCTGCCCAC ACTGAGCTGG GCTCCTCGAG GGGTGGGGCT      420

GCTGTCCCTG GAAGCCTGGC AGCAGCACTG TATCGGGTTG GCTGAAGCTG ARCGCCGTGG      480

GGTGCAGGGC TCCMGGAATC CCCGTTTGGC TGAAGGGGTT CCCTGTAGCC MGGGATGTTT      540

ATGAGGTCTC TCTGATGCCC CAGGCGCAGG ACATGTGTGC GGGTGGAGAA AAGCAGGCCC      600

TTTCAGTGCC AGCTCCACTC AATTTCTATG TGGACCAAGA ACGATAAACT TAAAAAATTT      660

TTTTTCCTAA GGTATCTTCA GAATATGGTG TATTTTTATG TGGAAAAGAA AAGTTATGAA      720

GGCAGCTGTT ACTTTAAGAG AAAATTCATT AAAAGTCCTC GAGGTATGAA GATGACGGCG      780

TGCTTCTCAA TCATTTTGGC ATAACTTGAT TGTGGCTGTA ATTTTTTTTT TTTTTTTTGT      840

CAAGCATGTC AGACAATAAA GTCTTTGTAA AAAGRGAAAA AAAAAAAAAA AAAAAAAAAA      900

ACTCGA                                                               906
```

(2) INFORMATION FOR SEQ ID NO: 191:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 1941 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

```
CTTCAGCTGA AGCCCAGGGA CCCCTTTTCC ACCCTGGGCC CCAATGCCGT CCTTTCCCCG      60

CAGAGACTGG TCTTGGAAAC CCTCAGCAAA CTCAGCATCC AGGACAACAA TGTGGACCTG     120

ATTCTGGCCA CACCCCCCTT CAGCCGCCTG GAGAAGTTGT ATAGCACTAT GGTGCGCTTC     180

CTCAGTGACC GAAAGAACCC GGTGTGCCGG AGATGGCTGT GGTACTGCTG GCCAACCTGG     240

CTCAGGGGGA CAGCCTGGCA GCTCGTGCCA TTGCAGTGCA GAAGGGCAGT ATCGGCAACC     300

TCCTGGGCTT CCTAGAGGAC AGCCTTGCCG CCACACAGTT CCAGCAGAGC CAGGCCAGCC     360

TCCTCCACAT GCAGAACCCA CCCTTTGAGC CAAYTAGTGT GGACATGATG CGGCGGGCTG     420

CCCGCGCGCT GCTTGCCTTG GCCAAGGTGG ACGAGAACCA CTCAGAGTTT ACTCTGTACG     480

AATCACGGCT GTTGGACATC TCGGTATCAC CGTTGATGAA CTCAKTGGTT TCACAAGTCA     540

TTTGTGATGT ACTGTTTTTG NATTGGCCAG TCATGACAGC CGTGGGACAC CTCCCCCCCC     600

CGTGTGTGTG TGCGTGTGTG GAGAACTTAG AAACTGACTG TTGCCCTTTA TTTATGCAAA     660

ACCACCTCAG AATCCAGTTT ACCCTGTGCT GTCCAGCTTC TCCCTTGGGA AAAAGTCTCT     720

CCTGTTTCTC TCTCCTCCTT CCACCTCCCC TCCCTCCATC ACCTCACGCC TTTCTGTTCC     780

TTGTCCTCAC CTTACTCCCC TCAGGACCCT ACCCCACCCT CTTTGAAAAG ACAAAGCTCT     840

GCCTACATAG AAGACTTTTT TTATTTTAAC CAAAGTTACT GTTGTTTACA GTGAGTTTGG     900

GGAAAAAAAA TAAAATAAAA ATGGCTTTCC CAGTCCTTGC ATCAACGGGA TGCCACATTT     960

CATAACTGTT TTTAATGGTA AAAAAAAAAA AAAAAATAC AAAAAAAAAT TCTGAAGGAC    1020

AAAAAAGGTG ACTGCTGAAC TGTGTGTGGT TTATTGTTGT ACATTCACAA TCTTGCAGGA    1080

GCCAAGAAGT TCGCAGTTGT GAACAGACCC TGTTCACTGG AGAGGCCTGT GCAGTAGAGT    1140

GTAGACCCTT TCATGTACTG TACTGTACAC CTGATACTGT AAACATACTG TAATAATAAT    1200

GTCTCACATG GAAACAGAAA ACGCTGGGTC AGCAGCAAGC TGTAGTTTTT AAAAATGTTT    1260

TTAGTTAAAC GTTGAGGAGA AAAAAAAAA AGGCTTTTCC CCCAAAGTAT CATGTGTGAA    1320

CCTACAACAC CCTGACCTCT TTCTCTCCTC CTTGATTGTA TGAATAACCC TGAGATCACC    1380

TCTTAGAACT GGTTTTAACC TTTAGCTGCA GCGNCTACGT CNAWCGNTGT GTATATATAT    1440

GACGTKGTAC ATTGCACATA CCCTTGGATC CCCACAGTTK GGTCCTCCTC CCAGCTACCC    1500
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444

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CTTTATAGTA TGACGAGTTA ACAAGTTGGT GACCTGCACA AAGCGAGACA CAGCTATTTA    1560

ATCTCTTGCC CAGATATCGC CCCTCTTGGT GCGATGCTGT ACAGGTCTCT GTAAAAAGTC    1620

CTTGCTGTCT CAGCAGCCAA TCAACTTATA GTTTATTTTT TTCTGGGTTT TTGTTTTGTT    1680

TTGTTTTCTT TCTAATCGAG GTGTGAAAAA GTTCTAGGTT CAGTTGAAGT TCTGATGAAG    1740

AAACACAATT GAGATTTTTT CAGTGATAAA ATCTGCATAT TTGTATTTCA ACAATGTAGC    1800

TAAAACTTGA TGTAAATTCC TCCTTTTTTT CCTTTTTTGG CTTAATGAAT ATCATTTATT    1860

CAGTATGAAA TCTTTATACT ATATGTTCCA CGTGTTAAGA ATAAATGTAC ATTAAATCTT    1920

GGTAAGACTT TAAAAAAAAA A                                              1941
```

(2) INFORMATION FOR SEQ ID NO: 192:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2118 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

```
AAATAATAAT AANAATAAAT AAAAATWAAG TGCTTAKTGT AACTCAGCGG ACAGGGCTCC     60

CAGCTGCTCT GGCACGTGGG ACACCYTCCA CCCTGCACAC AACAGGCATG CAAAGAGGAC    120

TGGATATGGT GGGGTAGAGT GCTTCTGGTG TGTTCACTTT AAGAAAACAT CTGCCAAGAG    180

AGAAGAGTGC CCAGGAAAGA CCAGGAAAAT ACAAGTACAT GGCTGCTTCA TACCATATAC    240

CCCAATTCTT TAAAGCAGCA AAAGGCACTT TTTTTTTCAG GCCAGAGTGA ATCTAAAACA    300

AACCTGGCTT TGCTTACAGG GAAGCTGTCC CAGAAGGACT GAGTGATGCC TCTTGTTCCC    360

TAAGGTCTGG AGAGTCTTTG CAAGTTTCCA ACGACATTTC CAACCAGGTG GGAGAGACCA    420

GCAGTTGACG AGACAAGTCA GACCCAAAAA ACGACGCCAA GGTAGTGAGT GGGTGCCTAT    480

TTGGGAGTAG GATGATTTGA GGAAACAGG AAGAAAAACC GGTCAGAAAG TGGCACTTTG    540

GAAGTGGAAA GCTGTTTGCA AATAGCAACT CTGGCTAAAG CGAAAATGTT AATCAAGTAG    600

AAAGTAAAAT TCAGGATCTT AGAAGCTCAT CCTTCTGATG AGAACTATTT TTTTTTCCGT    660

GAAGGAACTA TTATTACTTT AAAAGTGAGG GTAATTTACA TATGGGTGT ATATATTCTA     720

AAAATAGTAA TAAAAGTACC TTTTATAAGC AATGTTGTGT GGCTTGTAGA AGAAAGCAGG    780

GAGGAAAAAA AGGCAGGCAA AACTAGTCTA GGTCTAGGCC CTAAAAATGA GCTTCCTTCC    840

CACTTGACTG GAAACGCCCA TGTGATTTCT AGGCTGAAAA TAGGTAGGAT TTAACGAGTA    900
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ACCTAGTTCC CTTCTGTCTC TGATTTCTGA TCAGCTGATG GAGCTGCTAG TAAGAGGGGC        960

CGATCATGCT CCCAGACGAG TCCTTTGGCC TCTTGCTCTC CATCCCAAGC CTGACTCCTT       1020

CAGCAGCAGC CCCCTCCTTC TGTGTCCATC TGATGCAGGC AAGCAGGAGC AGTAAGAGGG       1080

CATCCCATGT TCCAGTTCAC CTTCTATGGG GTGACTARGA GGTTCCCGGT AACTAGGGCA       1140

GCCCARGCCC AGCAGGTTGC AAAAGCAGCT GCAAGCTTCA GAAACCCACT TCCTCCAACA  .    1200

CCAGGGAGGT GGCAGAGAGC CCATCCAAAA GCCCACTGGG AGAGGCATAA GATTCTGTGC       1260

CAGGCCCCCA GGTCCCCTCT GTGTCAGGTA GGCTCTGCTA CTGGCCTCTG AAGTAAAGGC       1320

AAANACAAAC GGGCAGGGCA GGGTGGCAGG AATAAAAAAC TCTGGACAGA AACCCTTTTA       1380

ATAAAGGAAA TTCCACCCCT CCCAATCCTT CCATGGAAGG GTGAGACCTT AATGTGATGT       1440

AAGAGGAAGG TCTTCTCTGG CTTTCAGGGA AACAGCTGCA GCTGAAACTT AGGGGCCCAT       1500

TCCAGGGCAC TTTTCACCAC AGCCAGTGCA GCCGCTCCAA GTGCCACTGT CAGCCCCATC       1560

ACTGCCAATT TCACAAAGCG GTTGGTCCTT GGCTTGGTCA GGACATCTTT TGTTCGATCT       1620

TCAGGCCGCA GAAGTCCCCG AANACCGCTG CCGCAGCACC ATATCAGGCC TCTGCTGGGC       1680

TGATGCCAGC TCAAAGTCTT TGAAAGTAGA GGCTGCCGTC CTCTCAGCTT GCTGTTGGGC       1740

AGCGGCCTCC CGAGCAAGTT CGGATGGGGG AAACTGAACA AAAAGGTCTC CTSTCTGCTG       1800

ATCAGTGTCT CATAGGGCAA GTCCTGAGGG ATCTGGGACA ACAGGTGGTG GACCGAGGCC       1860

ATGTCACAGT CACAGTCCAG GACTTCCTGC TCGCGATACA ACACAATCAC GGCTGCAAAG       1920

TAAATCGGCA TCAGTGGGTG GCAGGCCAGG AAGAAGTCAT ATAACCGCAC GACGTGCCTG       1980

AAGTCAGACA GGACATGCCC AAACCAGGTG ATGAGCCAGC TGAGGGCAAA GATGGTCCCT       2040

ACCTCAGCAC TCTGCATGAA GTCATGGAGC TCTGGATTCA CCTGGTCAAT GATGGGCATC       2100

AGATAGTTTA ATATATGC                                                    2118
```

(2) INFORMATION FOR SEQ ID NO: 193:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1538 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

```
CCGGGTTCGG CTCTGTGTCA GCAGCCGGGC GGCGCTCGGG CGGGACATGG CAGCCTGTAC         60

AGCCCGGCGG CCTGGCCGTG GGCAGCCGCT GGTGGTCCCG GTCGCTGACT GNGGCCCGGT        120

GGCCAAGGCC GCTCTGTGCG CGGCCGNAGC TGGAGCCTTC TCGCCAGCGT CGACCACGAC        180
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446

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GACGCGGAGG CACCTCTCGT CCCGAAACCG ACCAGAGGGC AAAGTGTTGG AGACAGTTGG        240

TGTGTTTGAG GTGCCAAAAC AGAATGGAAA ATATGAGACC GGGCAGCTTT TCCTTCATAG        300

CATTTTTGGC TACCGAGGTG TCGTCCTGTT TCCCTGGCAG GCCAGACTGT RTGACCGGGA        360

TGTGGCTTCT GCAGCTCCAG AAAAAGCAGA GAACCCTGCT GGCCATGGCT CCAAGGAGGT        420

GAAAGGCAAA ACTCACACTT ACTATCAGGT GCTGATTGAT GCTCGTGACT GCCCACATAT        480

ATCTCAGAGA TCTCAGACAG AAGCTGTGAC CTTCTTGGCT AACCATGATG ACAGTCGGGC        540

CCTCTATGCC ATCCCAGGCT TGGACTATGT CAGCCATGAA GACATCCTCC CCTACACCTC        600

CACTGATCAG GTTCCCATCC AACATGAACT CTTTGAAAGA TTTCTTCTGT ATGACCAGAC        660

AAAAGCACCT CCTTTTGTGG CTCGGGAGAC GCTAAGGGCC TGGCAAGAGA AGAATCACCC        720

CTGGCTGGAG CTCTCCGATG TTCATCGGGA AACAACTGAG AACATACGTG TCACTGTCAT        780

CCCCTTCTAC ATGGGCATGA GGGAAGCCCA GAATTCCCAC GTGTACTGGT GGCGCTACTG        840

TATCCGTTTG GAGAACCTTG ACAGTGATGT GGTACAGCTC CGGGAGCGGC ACTGGAGGAT        900

ATTCAGTCTC TCTGGCACCT TGGAGACAGT GCGAGGCCGA GGGGTAGTGG GCAGGGAACC        960

AGTGTTATCC AAGGAGCAGC CTGCGTTCCA GTATAGCAGC CACGTCTCGC TGCAGGCTTC       1020

CAGTGGGCAC ATGTGGGGCA CGTTCCGCTT TGAAAGACCT GATGGCTCCC ACTTTGATGT       1080

TCGGATTCCT CCCTTCTCCC TGGAAAGCAA TAAAGATGAG AAGACACCAC CCTCAGGCCT       1140

TCACTGGTAG GCCAGCTGAG GCCCCAAGTG CCCAGGCTTG GTCACCGGGA AGAACAACTC       1200

TCATCCCACA ATTGCTGCAG AACTCTTCTC TCCCCATCAT GGGCCACAGT GGGTCTCTTA       1260

ATTTGATTGT GGGGTTCTTT TTGTGGGGAG GGGTGGTATA ACTTTTCTTC AGAAGACCCA       1320

TGTGGGACAC CTCCAAGGCT GGCCTCCTCA TAAGCCCTGC CTACACCATG TTCCAGTAAA       1380

CCTCTCCACC AAGGAACTGT GTTCAGCTGC CACAGGCCTG GAGGAGTTTC CTGGCCTGTC       1440

ACGTGAGGTT TGATCAGTAA ACCAGTGCAS GYTTGGCCAA AAAAAAAAAA AAAAAAAAAA       1500

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAACTCGA                               1538
```

(2) INFORMATION FOR SEQ ID NO: 194:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1098 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

447

```
     AGACCCTGTC TCAAATAATA ATAATAATAA TAATCTTATT TTGGAGAATA AAGAGACCTS        60

     TGGATTTGAG GTGCCATTTG GGTAGAAAGA AAAGACGTTT ACACCGAGAA ATAGTCTGTG       120

5    TTGCCCTGAA GGAGCAGAGG GATGCATCGC TGGAGGTGAC CTACAGTTGA AGAAGACTCA       180

     TTATGACAGA CCTTGTCCTT CTTCCTTGTG GAAAGTGTTT CCTCTGCTGC TACTGCTCAT       240

     GAGACTCTTC CCCCTCCCTG TCCCAGGGAA CCAAAGGGCT TTNCTACCAC ACCCTTTCTT       300

10   NGCCCCCCGC CTCCCATGTC TGCTGTGCCT TTGTACTCAG CAATTCTTNG TTTGCTCCCA       360

     TTATCTTCCA GCCGGATACA GAGTGAATAG TTAACCACAC TTAGGTCAAA TAGGATCTAA       420

15   ATTTTTGTTC CTGCTCCNGT GTAAAGAGGC CAGTGTTTGT GTGTTGCAAG CAGCCTTGGA       480

     ATAGTAACTC TTCTCATTTG TTTGGGATCT GGCCAMCAAG TTCCAGAATG ATACACGGAT       540

     CAGTGCAGAA GTTCATCAGG CTCTCGGACC TTAGGGCTGT TGGAGAAGGC TTCAGCAGCA       600

20   GAACTGATGG TKAWKGYTCG TGTTCTCCAT CCTCAACTTT CTTTGCTTCG ATCATACACA       660

     AGAATACATT TGGAAGGGCA AAAAATGAAC ACTGTTGTTC ATTGCAGCCG TGTTTTGTGA       720

25   CACAGATGCA CAGTCTGCTG TGAAGACCTT CTCTCAAGTG GSATYTGGGA GTCCATGCCA       780

     GATCATGGTG CTTCATGAGA GACTGACAGC TATCAGGGGT TGTGGCACTT AGTGAGGACT       840

     CTCCTCCCCC AGTGTGTGCT GATGACACAT ACACACCTGA CAATAGCTTG AGTCTTCTCT       900

30   GTTCCTTTTA CTCTGTAGCC AACATACACA TGATTTAAAA CCCTTTCTAA ATATCTATCA       960

     TGGTTCATCC TTGTCCAAAT GCAGAGTCAG AGCTATTTGT ACTTCATTAT TATTTCCAAG      1020

35   GCGAATAGTT GGCTTTCTTT TTGCAAAAAT AATTAAAGTT TTTGTATGTT GCAAAAAAAA      1080

     AAAAAAAAAA CTACGTAG                                                    1098
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40

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     (2) INFORMATION FOR SEQ ID NO: 195:

             (i) SEQUENCE CHARACTERISTICS:
45                   (A) LENGTH: 1001 base pairs
                     (B) TYPE: nucleic acid
                     (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

50           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

     GAATTCGGCA CGAGATAGCT TGCATCTCAT CCCAGTAAAA CCACTTATTT ATAACATATC        60

     AACGTATTGA CAAGGTTGAA GAGCAAGATT GTTCTGAGGT GAGATGCAAA TTTCAAAGGG       120

55   GTGAGCACTA ATTGTTCCAG TGATTGTTTA TTTATTGGCT AGGACATAAT TACTCTCTTT       180

     GAGGTTACAC ATCTGCCTCC AGGTTCCTGT GTGCTTGTGC CCTTGGGATC AGGCCAGGGC       240

60   AGACTGTGAT CACTGAGATT CAAACTCCCA GARTAATCAG CAAGAGCTTT CTAGAGACCA       300
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AGGCCAGGCC TGATCCCTGA GGGATGCATG AGAAGGCTTG GAATCTCATT CTGCTATGGT      360

GGCTCTCTCT TGATCTTCTT GGAGTAGCAA AAACAGCAAT GTGGGCCCAA TGGTGTGGCC      420

TAAATGATCA CAAAGGTAAA TGAGTAAAGG GCTCAGCAGA TGAGTAAGGA GCCTTGTCCT      480

GAGAAATTAG CACTGGGCTC TGCATTCAGA AACATGTGAT AAGCATTGCC CATTGCACAT      540

TGCCTTTATT GTGTAAGGAC ATGAAATTCC AGTTTTGCAT AGCTAGTGAT GAATACCTGA      600

AGGGAATTGC AGACATATTT TATTTTATTT TTAATTGACA GATGGAATTG TATATATTTA      660

TCATGTACAT AATCATGCTT TAAAATATGT ACATTATGGA ATGGCTAAAT CAAACTAACC      720

TAGGCATTAT CTCATATAAT TGTCATTTTT GTGGCGAGAA GACTAAAAAT CTACCCTTTC      780

AGCATTTTTA AAGAATACAA TGTGTTTTAT TAACAACAGT CACCATTTGG TACACTAGAT      840

CTCTTGAACT TCTTCCTCTT ATCTAACTGA GATCTTGTAA CCTTTGATAA CAGCTCCCAA      900

GCCCTTCCCC AACCACTGCT CCACCCGTGG TAACCACCAT TCTATTCTCA ACTTCCTGGT      960

AATCACCATT CTAGACACAG GGAAGACTCT CTACCCTCTG A                        1001
```

(2) INFORMATION FOR SEQ ID NO: 196:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1443 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

```
ATAAACTGAA ATAGGTCATG CAAATATAAA ATATTATTTT TAAATTATTT GTCATAAGAA       60

ACGATGGTGG CCATATTTTG CTTTAATAAT GGAAAAAATG TGGTTAGCAT TCTKTGGAAG      120

GTGGTCATCA GATAGTAGAC ATTTTCTAGG ATTTATTTCT ACCTGCATAT GTGGAAATGT      180

GTACTACTTT AGATTTATWT AATGGCAGCT AACTCAGAGG CATCAAAATG TGCTAATGGT      240

GTAATATGGC CTTTGTCTTG CTGTYCTGTT TTGTARGCCT TCAATCAAGC ARGGGCAGGG      300

CCGTACAGTG AACTTGTCCT TTGSCAGACG CCAGCGTCTG CCCCTGACCC GTCTCCACT       360

CTCTGTGTCC TGGAGGAGGA GCCCCTTGAT GCYTACCCTG ATTCACCTTC TGCGTGCCTT      420

GTACTGAACT GGGAAGAGCC GTGCAATAAC GGATCTGAAA TCCTTGCTTA CACCATTGAT      480

CTAGGAGACA CTAGCATTAC CGTGGGCAAC ACCACCATGC ATGTTATGAA AGATCTCCTT      540

CCAGAAACCA CCTACCGGTG AGTGCAAGGG AGTAGAAATC TGCATCAGCA CATCAGCACT      600

TGGGGATCTA AGTAAACCTC TCGGGGAAAA TGACCAAGTG GATGTCATCT CCCAGCTGTT      660
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TCTAAGAGCC CAGATGTCCA GAGTATTGTC TCACCTTGAT CCCTCAGGCC AGAAGACCTG   720

TGAAAAAGCC ACACTGGTTC AGGGACTCAC TGGACGGTTT TGTGTCCACT TTAACTTGCA   780

CCGTCTCTAC CCCAGAGTGG ACTCARATCC TCAAGTCATC CTCTGAACAT TGTTGTCAGA   840

AATTATAAAA GGGCTTTGGC AATATGTTAG CCCAAGAATT TGGCTTCTTC CAGAAATTGT   900

GCCGACNTTA ACAGTGGCTT AAATGATGGT AAAACTTTTA AGATTTCTAA AAGGTTGGCA   · 960

TTGGAGATAC GTTGACTTTT ATTAAACMAC CTATAGTTGT TTAATGATTT CTAAAAAAT   1020

ATCTGGAGCT CAGGGGTTCA ACTGAGGGAA CACATGTTGA GRATCATTGT TTATTAATTA   1080

AATGCCAGGT AACCCGTTGA AATTATCAAA AACATCTTCC ACGTACCAGA AAGCACCTCA   1140

GAGGATAGTT CTGTTATGGA GAAGATGAAA TGGTTTAGTA GTGTAGGAAC TATGGAAAGG   1200

TGAGCTTAGA TTTGGATAGT AAAACCTCAA GACCCTACTT AAAAAGTATT TTATGAATGC   1260

AGCATAAATA ATTTAATTCA GTGTTAANAT GCCAAGGCTA GTATATTGAG CTGAATGTGA   1320

AAAGAAACTC ACATTGGGAG AATGCCACCT TTTCCTTATA AGATAGCTTT GAAGATACCA   1380

TTTTAGACAG ATGGAAATTG AATAGCTTTA GAAAAGGCAA ATGTTTGATC TTGGGGAAAA   1440

AAA   1443

(2) INFORMATION FOR SEQ ID NO: 197:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1282 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

GAAAAAAAAA AGTATGACCC AGTAGCTAGG CACCTGTGGC CCCGCCAAGT TGACACATAA   60

AATTAACTGT CACAGTATCA TCTTAGAAGT GAAAGAAGCC CCTTTATCCT GCAGTGCCCC   120

TCTACCACCA CCTACTGACA AAGAACATGG TGCTATCTGG CATGGGAGAA ATGTTCAGTT   180

TGCTATGGCT TGTATGTGTC CCCTCAAATT CAAGTGTTGC CAATGTGACA GCATCAAGAG   240

GTGGGGTCTT TAAGAGATCA CTAGGCCATG AGGGATTCTC TTAGGACTGG GATGAAGGCC   300

CATAATAAAA GAGGTTTCAG GGAGCATCCT GCTAGCTTGC CTTCTGTATG TGAGAACACA   360

GCAAGAAAGC CCTAGTCAAC AAGTGCCAGC TCCTTGATCT TAGACTTCCC ACCTCCAGA   420

ACTGTGAGAA ATACATTTCT GTTCCTTACA AATTACCCAG TCTCCTGTAT TCTGTTATAG   480

CAGCACAAAA TGAAGATACC ATACCTGAAC ACCTGAACAT TCTTCACAG GTAGTAAATG   540

CACTGCTTTA TTCTGGTCTC AGTATTGTGT GCTTAATAAG GAAATGAGAA AGGTGGATC   600

450

AGGGCATAGG ATGAACAAGT TACTGCTAGA CCTCTCACHA TGCCACTAAT GGATAAGATT   660

GTATTTTCAT CATTNCTTGT CTCTTCGGAA GCTAACACTA TGCTATAATA GGCATTAAAT   720

AGATGTCTAA AAACACCTTA AGTATTTGTC TAGAAATCTG GTGCATTGTC CAGAAAGAAC   780

CAAAATTCMA AATAATTTCA AAGGGCCTAA AGCACTANTT AATCMGAATT CATTAGTTTT   840

TAATGGTACT ACCACTCTCA AATTTAAAAT GTCATCTTAC GTTCCTCTTC CTCGCATTGG   900

ATTTATTGCT AAAACCTGGT AAACACTTTA ATCCYTTTCA ATTCCATTAC CACTGCTCTT   960

GTCCAGAATT ACTCGCAGAC TAATAGTCAC CTGACTTCTC CCCCTGCATC CCGATTTGCT   1020

GTCTAATTCT GGTTACAAAT AAGTAACTGC CAAACTAATC TTTCTAAAAA GCAAGACTGA   1080

TCTCGTCACT CCTTTGCTCA ACAATGTAAA AGCTCCCATT GTCTCCCAAA TAAAACCAGC   1140

TTTCCACTGT GTATACAATA CATCCATGAT CTGTATCCAG CATCATTTTG TATTTGCTCA   1200

CTTTATACAC CACCCCCCAT GCCACATCAA ATTAAATTAT CCTGATAAAT GCAACTGCAA   1260

AAAAAAAAAA AAAAAAACTC GA   1282

(2) INFORMATION FOR SEQ ID NO: 198:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 951 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

ATTTCGGAAC GAGGACTGAA GTGGGAGCGG CGGCAGGGTA GAAGACAGAA GGGGGATCTA   60

TGTGGTAACT AAAGAATGTT TCTGTTTTGT TAATTATTGT GTGTGTGTGG TTTTATTGTT   120

TGCTTAAGAG AATCAAAAAC TGAAAAAAAT GAGAATACAG GAAATGGCTC TTGTTTATTT   180

TTTTGCTGTG TTTACAGCTT GTTAATGCTC TACTGTCTTT GTTTCAAGAG AGATTGTTC   240

ACTGCCCAGC TCGTTTTGTG TCCTGAGCCC TATGCCCAGC CCACCTTATA AATCATGCCT   300

GTTTAGATGT TTGATTTTGT TCTGTTTGCT ATTGTTATCT TAAAGGTGTA TAACTCTGAC   360

ATGCCAGACA TCAAATTAAG CTCAAATTAA GCTCTCGTTT AAATGTTTAA ACACCTAATT   420

TATATTCTAA TTGATCCCAG CCACTGATGC ATGTACTTTA GCTACTTCTG CTAAATAAGC   480

ATATTAATTT TCCACATCAG GCCATCAGAT CTTGAGAACC AACAGTTATC TAGAATTCCG   540

TGTCTACTAA TGTTTCACCT GCATGCAGCC TTCATTAATT TTGTAGCAAA ATATAAAGTG   600

ATCATTATGT AGTTTCTGGA TTAAAAAAAT TTGTGTGTGA AGTTGCTTTG TAAAGTGCAT   660

451

GTGGAATTAA TGGGACAGTG TGCCCTTTGT GTTAGATGTT AGAGCAAAAG AAAGGGCTTA   720

TAGTGTTAGT ATTGGAGCAC TTTGAAGATA GATATTTTCA GAAAAGATGT AGGATTTAAA   780

AGTTAAATTT TAAATTTTAG AAAAAGATAT GATGGCAATT GGAAATAGTC ACAATGAAGT   840

TCTTCATCCA GTAGGTGTTT AACAGTGTTA TTTTGCCACT GGTAATGTGT AAACTGTGAG   900

TGATTTACAA TAAATGATTA TGAATTCAAA AAAAAAAAAA AAAAAACTCG A   951

(2) INFORMATION FOR SEQ ID NO: 199:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1740 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

TTATTATAAT AATGATGATG ATTCCAAGGA AAAAACCTAC AGCGAATGTT CCATTTCTAC   60

CCCGCACGCA GACACTCTCC CTAACACTGA TAACCTGAGC CCCCAGCACT GGACGGAAGA   120

ATGCTGGCGT CTCCGTGTGT ACTGGTTCAG GGTTCTGGCC CCAGCCTTGT CAGGACCCCC   180

TGGTGTCCAG AGCCCCCACC CCTCCCGCAA CAAGCAGCTG ATGCCCCAGT GATTCTCTAT   240

ACATTTTTCA CCTCGGCCAA TATGTCCAGG AAAACTGCTT ACTTCTCTTT TCTTGCCTGG   300

AGCCTTCATT GTTCACCCTT ACGTTGCAAT ATAGGAATTA ATGCTACAAA ATAAAAGTAA   360

AGCTTACCTG AAAAGTGCAT AGTTTGGGGC AATGGTATCT ACATCTCCCA CTGTGGGAAA   420

ACCAGCAAAG CATCAAAACT CTCAATTCTC CTGTTACCRA ATGCAGATCT GAATTATAAG   480

ATGTTTATGT TTGACCATTG TTTCAACAAT GGGATTTTGT TACGAATTAT CCCTTTAACT   540

GAAACCCTCA GTTTTACTGT TTACATTATT AGGAAAACAG GGATATCTTT TGAATCTAAA   600

AATTTGATGT ACAGCATGTG ATTTTTGAAG TTTACATGTA AAGTCACAGT ATAGGTGAAA   660

TAACGTTTGT CATATTTTGA GACGTATCCT GCAGCCATGT TTTTACGTGA GTGTTTTAGT   720

CAAAGTACAT GGTAGACAGT CTTTCACAAT AAAAGGAAAA GGATTTTTTT TCCTCCAAAT   780

GTACATTTAT CAACCTAATG ATTGATTTTT TTAAAAAGAG ATTTCGCCCC AGTCTGGTTT   840

ATGAAAGTTC ATTGCCCTAA ACTGTGCTGA TTGTTTTTAA TCAAGTTATA AATTTCCAAC   900

CTAGATCATG TATCTACCAA CTCTCCTGCA TTTTCCAAAA GGCATTGAGC TTAAATATTA   960

GTCTTGCTTA GAGTAGGTTA TCCACTTACA TGCTGCGCTA AAGCCATGCC TTTGAAACTC   1020

CTTGTTTAAA ACATGATATG ATTTTTGTGG GCAGTTTCAG AAAAGAAAAC AAACAAACAA   1080

AAATCGACCC TTTAATTATT ACTTGCAACT CAACAGATCT CCCTGCCGTA CTGCCTTTTC   1140

CAGGAACTTT ACTTCAGGGC TGTCCAGATT GCAGTTGTGC CCCGTGTATG TGGATCTAGT   1200

TCACAGAGTC TTTGGAAGCC AGCAGTCGTG CCCTCCGTAT ACTGTCCACT CATTTTATGT   1260

AGATTTGGTA TCCTCAGCAG CCAGTGTTAA CACCACTGTC ACGTAGTTAN CAGATTCATC   1320

TTTTATGTAT TTAAAGTAAT CCATACTATG ATTTGGTTTT TCCCTGCACC ATTAATTCTG   1380

GCATCAGATC AGTTTTTGTG TTGTGAAGTT CTACTGTGGT TTGACCCAAG ACCACAACCA   1440

TGAGACCCTG AAGTAAAGAT AAGGTACACA TACATTATTT GAGTAACTGT TTCCTTGGGG   1500

GCCAATCTGT GTATGCTTTT AGAAGTTTAC AGAATGCTTT TATTTTTGTC TATAACAAAC   1560

AGTCTGTCAT TTATTTCTGT TGATAAACCA TTTGGACAGA GTGAGGACGT TTGCCCTGTT   1620

ATCTCCTAGT GCTAACAATA CACTCCAGTC ATGAGCCGGG CTTTACAAAT AAAGCACTTT   1680

TGATGACTCA MAAAAAAAAA AAAAAAAAMC YCGGGGGGGG GCCGGTAACC CATTTNNCCC   1740

(2) INFORMATION FOR SEQ ID NO: 200:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1707 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

GCTTATAGAA GGGAGAGGAG CGAACATGGC AGCGCGTTGG CGGTTTTGGT GTGTCTCTGT   60

GACCATGGTG GTGGCGCTGC TCATCGTTTG CGACGTTCCC TCAGCCTCTG CCCAAAGAAA   120

GAAGGAGATG GTGTTATCTG AAAAGGTTAG TCAGCTGATG GAATGGACTA ACAAAGACC   180

TGTAATAAGA ATGAATGGAG ACAAGTTCCG TCGCCTTGTG AAAGCCCCAC CGAGAAATTA   240

CTCCGTTATC GTCATGTTCA CTGCTCTCCA ACTGCATAGA CAGTGTGTCG TTTGCAAGCA   300

AGCTGATGAA GAATTCCAGA TCCTGGCAAA CTCCTGGCGA TACTCCAGTG CATTCACCAA   360

CAGGATATTT TTTGCCATGG TGGATTTTGA TGAAGGCTCT GATGTATTTC AGATGCTAAA   420

CATGAATTCA GCTCCAACTT TCATCAACTT TCCTGCAAAA GGGAAACCCA AACGGGGTGA   480

TACATATGAG TTACAGGTGC GGGGTTTTTC AGCTGAGCAG ATTGCCCGGT GGATCGCCGA   540

CAGAACTGAT GTCAATATTA GAGTGATTAG ACCCCCAAAT TATGCTGGTC CCCTTATGTT   600

GGGATTGCTT TTGGCTGTTA TTGGTGGACT TGTGTATCTT CGAAGAGTAA TATGGAATTT   660

CTCTTTAATA AAACTGGATG GGCTTTTGCA GCTTTGTGTT TTGTGCTTGC TATGACATCT   720

GGTCAAATGT GGAACCATAT AAGAGGACCA CCATATGCCC ATAAGAATCC CCACACGGGA   780

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CATGTGAATT ATATCCATGG AAGCAGTCAA GCCCAGTTTG TAGCTGAAAC ACACATTGTT        840

CTTCTGTTTA ATGGTGGAGT TACCTTAGGA ATGGTGCTTT TATGTGAAGC TGCTACCTCT        900

GACATGGATA TTGGAAAGCG AAAGATAATG TGTGTGGCTG GTATTGGACT TGTTGTATTA        960

TTCTTCAGTT GGATGCTCTC TATTTTTAGA TCTAAATATC ATGGCTACCC ATACAGCTTT       1020

CTGATGAGTT AAAAAGGTCC CAGAGATATA TAGACACTGG AGTACTGGAA ATTGAAAAAC       1080

GAAAATCGTG TGTGTTTGAA AAGAAGAATG CAACTTGTAT ATTTTGTATT ACCTCTTTTT       1140

TTCAAGTGAT TTAAATAGTT AATCATTTAA CCAAAGAAGA TGTGTAGTGC CTTAACAAGC       1200

AATCCTCTGT CAAAATCTGA GGTATTTGAA AATAATTATC CTCTTAACCT TCTCTTCCCA       1260

GTGAACTTTA TGGAACATTT AATTTAGTAC AATTAAGTAT ATTATAAAAA TTGTAAAACT       1320

ACTACTTTGT TTTAGTTAGA ACAAAGCTCA AAACTACTTT AGTTAACTTG GTCATCTGAT       1380

TTTATATTGC CTTATCCAAA GATGGGGAAA GTAAGTCCTG ACCAGGTGTT CCCACATATG       1440

CCTGTTACAG ATAACTACAT TAGGAATTCA TTCTTAGCTT CTTCATCTTT GTGTGGATGT       1500

GTATACTTTA CGCATCTTTC CTTTTGAGTA GAGAAATTAT GTGTGTCATG TGGTCTTCTG       1560

AAAATGGAAC ACCATTCTTC AGAGCACACG TCTAGCCCTC AGCAAGACAG TTGTTTCTCC       1620

TCCTCCTTGC ATATTTCCTA CTGAAATACA GTGCTGTCTA TGATTGTTTT TGTTTTGTTG       1680

TTTTTTYGAG ATCACGYTAC TGGGCTC                                           1707
```

(2) INFORMATION FOR SEQ ID NO: 201:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 779 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

```
CTGTCCCCAG TGTTTCCAGG TAATGACTTG GCACTCCAGA GAAAGTTTCA TRCTGTTGCG         60

TGTGGTGGCT CCAAGCCAAG CACCTGGCAT GCAGGTCAGC CCTTCCCAGC GGGCGTGGCG        120

TCGTCCTCTT CACAGATGCC ACGTTGCAGC CCCAAGGCCT CACCATTTTG CGTTTTTTAG        180

AAACCCATTT TCTTGGTCAT TTATAAAGCT GCTTTATAGA TATCTTTGAT CCTGGCATGC        240

CTTGGTTTCC TCTCCCTTCC CTCTTTCCAA TCCTGGTTTC CTAACCTCCT CTTGTAGTAA        300

TTCTCAACTC AACTCAAAGT CCCAAGAATT TGGAATGGTA GGATGCTGTG CGGGGAGCTC        360

GAGGCTGAGG CATAATCACT GCTTCGGTTC TGCTCATCAG GGGACACGCT CCCTTACTCA        420

TGGCAGCCAT GTTTGATTGT CACAGAGCCC CCCGAATACT CTGTCTATAG TGACACACTG        480
```

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          TAGGTGTCAT AAATTTTAAG AAACCTGCTT TTAAGTACTA TTTATAGGTT TTTCTGTTAT        540

          ACTTGCAACC TAGTTTTAAA ATACATGAGG ATTTTATGAA AGCTTTATAC AGACATTTAT        600

  5
          AGGAAACTCA TTCTTTGATT TTAGGTGCCA TTTAAATTGA TAACACTTAC TTTATAAAAA        660

          GATGCTTTTT GTCTGGATAG AGCCTTATAG TTTAAAATAT CTTCATATAT TGCCATTTGA        720

 10       TCAAATAAAT TTCTTACTTA GAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAACTCGA         779
```

15   (2) INFORMATION FOR SEQ ID NO: 202:

                 (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 1617 base pairs
                     (B) TYPE: nucleic acid
 20   (C) STRANDEDNESS: double
                     (D) TOPOLOGY: linear

              (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

```
 25       GGCACAGCTT TCTGTCTCTT CCTCGCTCCC TCTCTTTCTC TCCTCCCTCT GCCTTCCCAG         60

          TGCATAAAGT CTCTGTCGCT CCCGGAACTT GTTGGCAATG CCTATTTTTT GGCTTTCCCC        120

          CGCGTTCTCT AAACTAACTA TTTAAAGGTC TGCGGTCGCA AATGGTTTGA CTAAACGTAG        180
 30
          GATGGGACTT AAGTTGAACG GCAGATATAT TTCACTGATC CTCGCGGTGC AAATAGCGTA        240

          TCTGGTGCAG GCCGTGAGAG CAGCGGGCAA GTGCGATGCG GTCTTCAAGG GCTTTTCGGA        300

 35       CTGTTTGCTC AAGCTGGGCG ACACATGGCC AACTACCCGC AGCCTGGGAC GACAAGACGA        360

          ACATCAAGAC CGTGTGCACA TACTGGGAGG ATTTCCACAG CTGCACGGTC ACAGCCCTTA        420

          CGGATTGCCA GGAAGGGGCG AAAGATATGT GGGATAAACT GAGAAAAGAA TCCAAAAACC        480
 40
          TCAACATCCA AGGCAGCTTA TTCGAACTCT GCGGCAGCGG CAACGGGGCG GCGGGGTCCC        540

          TGCTCCCGGC GTTCCCGGTG CTCCTGGTGT CTCTCTCGGC AGCTTTAGCG ACCTGGCTTT        600

 45       CCTTCTGAGC GTGGGGCCAG CTCCCCCCGC GCGCCCACCC ACACTCACTC CATGCTCCCG        660

          GAAATCGAGA GGAAGATCCA TTAGTTCTTT GGGGACGTTG TGATTCTCTG TGATGCTGAA        720

          AACACTCATA TAGGATTGTG GGAAATCCTG ATTCTCTTTT TTATTTCGTT TGATTTCTTG        780
 50
          TGTTTTATTT GCCAAATGTT ACCAATCAGT GAGCAAGCAA GCACAGCCAA AATCGGACCT        840

          CAGCTTTAGT CCGTCTTCAC ACACAAATAA GAAAACGGCA AACCCACCCC ATTTTTTAAT        900

 55       TTTATTATTA TTAATTTTTT TTGTTGGCAA AAGAATCTCA GGAACGGCCC TGGGCACCTA        960

          CTATATTAAT CATGCTAGTA ACATGAAAAA TGATGGGCTC CTCCTAATAG GAAGGCGAGG       1020

          AGAGGAGAAG GCCAGGGGAA TGAATTCAAG AGAGATGTCC ACGGACGAAA CATACGGTGA       1080
 60
```

455

ATAATTCACG CTCACGTCGT TCTTCCACAG TATCTTGTTT TGATCATTTC CACTGCACAT   1140

TTCTCCTCAA GAAAAGCGAA AGGACAGACT GTTGGCTTTG TGTTTGGAGG ATAGGAGGGA   1200

5   GAGAGGGAAG GGGCTGAGGA AATCTCTGGG GTAAGAGTAA AGGCTTCCAG AAGACATGCT   1260

GCTATGGTCA CTGAGGGGTT AGCTTTATCT GCTGTTGTTG ATGCATCCGT CCAAGTTCAC   1320

TGCCTTTATT TTCCCTCCTC CCTCTTGTTT TAGCTGTTAC ACACACAGTA ATACCTGAAT   1380

10 ATCCAACGGT ATAGATCACA AGGGGGGGAT GTTAAATGTT AATCTAAAAT ATAGCTAAAA   1440

AAAGATTTTG ACATAAAAGA GCCTTGATTT TAAAAAAAAA AGAGAGAGAG ATGTAATTTA   1500

15 AAAAGTTTAT TATAAATTAA ATTCAGCAAA AAAAGATTTG CTACAAAGTA TAGAGAAGTA   1560

TAAAATAAAA GTTATTGTTT GAAAAAAAAA AAAAAAAAAW CTCGACCGCA AGGGAAT   1617

20

(2) INFORMATION FOR SEQ ID NO: 203:

25   (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 1974 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

30   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

GAATTCGGCA CGAGGCTGAG GGAGCTGCAG CGCAGCAGAG TATCTGACGG CGCCAGGTTG   60

CGTAGGTGCG GCACGAGGAG TTTTCCCGGC AGCGAGGAGG TCCTGAGCAG CATGGCCCGG   120

35 AGGAGCGCCT TCCCTGCCGC CGCGCTCTGG CTCTGGAGCA TCCTCCTGTG CCTGCTGGCA   180

CTGCGGGCGG AGGCCGGGCC GCCGCAGGAG GAGAGCCTGT ACCTATGGAT CGATGCTCAC   240

40 CAGGCAAGAG TACTCATAGG ATTTGAAGAA GATATCCTGA TTGTTTCAGA GGGGAAAATG   300

GCACCTTTTA CACATGATTT CAGAAAAGCG CAACAGAGAA TGCCAGCTAT TCCTGTCAAT   360

ATCCATTCCA TGAATTTTAC CTGGCAAGCT GCAGGGCAGG CAGAATACTT CTATGAATTC   420

45 CTGTCCTTGC GCTCCCTGGA TAAAGGCATC ATGGCAGATC CAACCGTCAA TGTCCCTCTG   480

CTGGGAACAG TGCCTCACAA GGCATCAGTT GTTCAAGTTG GTTTCCCATG TCTTGGAAAA   540

50 CAGGATGGGG TGGCAGCATT TGAAGTGGAT GTGATTGTTA TGAATTCTGA AGGCAACACC   600

ATTCTCCAAA CACCTCAAAA TGCTATCTTC TTTAAAACAT GTCAACAAGC TGAGTGCCCA   660

GGCGGGTGCC GAAATGGAGG CTTTTGTAAT GAAAGACGCA TCTGCGAGTG TCCTGATGGG   720

55 TTCCACGGAC CTCACTGTGA GAAAGCCCTT TGTACCCCAC GATGTATGAA TGGTGGACTT   780

TGTGTGACTC CTGGTTTCTG CATCTGCCCA CCTGGATTCT ATGGAGTGAA CTGTGACAAA   840

60 GCAAACTGCT CAACCACCTG CTTTAATGGA GGGACCTGTT CTACCCTGG AAAATGTATT   900

TSCCCTCCAG GACTAGAGGG AGAGCAGTGT GAAATCAGCA AATGCCCACA ACCCTGTCGA   960

AATGGAGGTA AATGCATTGG TAAAAGCAAA TGTAAGTKTT CCAAAGGTTA CCAGGGAGAC   1020

CTCTGTTCAA AGCCTGTCTG CGAGCCTGGC TGTGGTGCAC ATGGAACCTG CCATGAACCC   1080

AACAAATGCC AATGTCAAGA AGGTTGGCAT GGAAGACACT GCAATAAAAG GTACGAAGCC   1140

AGCCTCATAC ATGCCCTGAG GCCAGCAGGC GCCCAGCTCA GGCAGCACAC GCCTTCACTT   1200

AAAAAGGCCG AGGAGCGGCG GGATCCACCT GAATCCAATT ACATCTGGTG AACTCCGACA   1260

TCTGAAACGT TTTAAGTTAC ACCAAGTTCA TAGCCTTTGT TAACCTTTCA TGTGTTGAAT   1320

GTTCAAATAA TGTTCATTAC ACTTAAGAAT ACTGGCCTGA ATTTTATTAG CTTCATTATA   1380

AATCACTGAG CTGATATTTA CTCTTCCTTT TAAGTTTTCT AAGTACGTCT GTAGCATGAT   1440

GGTATAGATT TTCTTGTTTC AGTGCTTTGG GACAGATTTT ATATTATGTC AATTGATCAG   1500

GTTAAAATTT TCAGTGTGTA GTTGGCAGAT ATTTTCAAAA TTACAATGCA TTTATGGTGT   1560

CTGGGGGCAG GGGAACATCA GAAAGGTTAA ATTGGGCAAA AATGCGTAAG TCACAAGAAT   1620

TTGGATGGTG CAGTTAATGT TGAAGTTACA GCATTTCAGA TTTTATTGTC AGATATTTAG   1680

ATGTTTGTTA CATTTTTAAA AATTGCTCTT AATTTTTAAA CTCTCAATAC AATATATTTT   1740

GACCTTACCA TTATTCCAGA GATTCAGTAT TAAAAAAAAA AAAATTACAC TGTGGTAGTG   1800

GCATTTAAAC AATATAATAT ATTCTAAACA CAATGAAATA GGGAATATAA TGTATGAACT   1860

TTTTGCATTG GCTTGAAGCA ATATAATATA TTGTAAACAA AACACAGCTC TTACCTAATA   1920

AACATTTTAT ACTGTTTGTA TGTATAAAAT AAAGGTGCTG CTTTAGTTTT CTGA   1974

(2) INFORMATION FOR SEQ ID NO: 204:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1057 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CGGCCTTCCG GGGCAACCGT TCGTCCCAAC NCGGGAAAGG GTCCTGGAGN CGGGAACTAG   60

GAGCCTCGGA AGTCCAAGGG CGGAGCGCCC TTTGCTAATA AGCCAATCAG AACGTGAGAC   120

GCTCCGGTGG GNCGGTGCCG TCGAGCGCGG GGTGGAGTCT GGGTGACTTG GCTGGCGGGA   180

TCAAGTGCAG CTGCTTCAGG CTGAGGTGGC AGATAGTGAG CGCTGGTGGC GGAGTTAAAG   240

TYAAAGCAGG AGAGTAATWA TGAATAGCGC AGCGGGATTC TCACACCTAG ACCGTCGCGA   300

457

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GCGGGTTCTC AAGTTAGGGG AGAGTTTCGA GAAGCAGCCG CGCTGCGCTT CCACACTGTG    360

CGCTATGACT TCAAACCTGC TTCTATTGAC ACTTCTTCTG AAGGATACCT TGAGKTTGGC    420

GAAGKTGAAC AGKTGACCAT WACTCTGCCM AATATAGAAA GTTGAAGGAA GCAGTAAAAT    480

TCAGTATCGT AAAGAACAAC AGCAACAACA ATGTGGAATT CASCCAGGAC TCCCAATCTT    540

GTAAAACATT CTCCATCTGA AGATAAGATG TCCCCAGCAT CTCCAATAGA TGATATCGAA    600

AGAGAACTGA AGGCAGAAGC TAGTCTAATG GACCAGATGA GTAGTTGTGA TAGTTCATCA    660

GATTCCAAAA GTTCATCATC TTCAAGTAGT GAGGATAGTT CTAGTGACTC AGAAGATGAA    720

GATTGCAAAT CCTCTACTTC TGATACAGGG NAATTGTGTC TCAGGACATC CTACCATGAC    780

ACAGTACAGG ATTCCTGATA TAGATGCCAG TCATAATAGA TTTCGAGACA ACAGTGGCCT    840

TCTGATGAAT ACTTTAAGAA ATGATTTGCA GCTGAGTGAA TCAGGAAGTG ACAGTGATGA    900

CTGAAGAAAT ATTTAGCTAT AAATAAAAAT TTATACAGCA TGTATAATTT ATTTTGTATT    960

AACAATAAAA ATTCCTAAGA CTGAGGGAAA TATGTCTTAA CTTTTGATGA TAAAAGAAAT    1020

TAAATTTGAT TCAGAAAAAA AAAAAAAAAA AACTCGA                             1057
```

(2) INFORMATION FOR SEQ ID NO: 205:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 721 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

```
GAATTCGGCA CGAGTCATCC CTCTCCCTCT TTCACTCCCT TACTCTTACT CTGTTTTTTG     60

TGCTCCAGAC AGACAGACCC TACCTCTTTT GCTTCTTTTT TGTTTGTTTG TTTTGAGATG    120

GAGTGTCGCT CTTGTTGCCC AGGCTGGAGT GCAGTGGCGC AATCTCGGCT CACCACAACC    180

TCTGCCTCCC GGGTTCAAGC AATTCTCCTG CCTCAGCCTC CCGAGAAGCT GGGGATTACA    240

GGCATGCGCC ACCACACCCA GCTNAATTTT ATATTTTTAG TAGAGATGGT GTTTCTCCAT    300

GTTGGTCAGG CTGGCCTCAA ACTCCCAACC TCAGGTGATN CCGCCTGCTT TGGCCTCCCC    360

AAAGTGCTGG GATTACAGGC GTGAGCCACT GCGCCCAGCC TCTTTTGCTC CTTTATACTC    420

ATTAACTCAC GCCTGTAATC CCTGTTTTGG GAGGCCAAAG TGAGAAGGTT GCTTGAGGCC    480

AAGAGTTTGA GACTAGCCTG GCAACACAG CAAGATGCCA TCTTTATAAT AAAAATAAAA    540

ATAAAAATCA ATTAGCTGGG CATGGTGGAA CGCACCTGTA GTCCCAGCCA ATTGAGAGGC    600

TGAAGTGGGA GGATCATTGA GCCCAGGAGT TGAGGTTGCA GTGAGCCATG ATCATGTCAC    660
```

458

```
        TACACTCAGC CTGGGCAATA GAGGGACATG TTGTCTCTAA AAAAAAAAAA AAAAAACTCG    720

        A                                                                    721
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(2) INFORMATION FOR SEQ ID NO: 206:

            (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 2465 base pairs
                  (B) TYPE: nucleic acid
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

```
        CCACCATTTA TCCAACTGAA GAGGAGTTAC AGGCAGTTCA GAAAATTGTT TCTATTACTG    60

        AACGTGCTTT AAAACTCGTT TCAGACAGTT TGTCTGAACA TGAGAAGAAC AAGAACAAAG    120

        AGGGAGATGA TAAGAAAGAG GGAGGTAAAG ACAGAGCTTT GAAAGGAGTT TTGCGAGTGG    180

        GAGTATTGGC AAAAGGATTA CTTCTCCGAG GAGATAGAAA TGTCAACCTT GTTTTGCTGT    240

        GCTCAGAGAA ACCTTCAAAG ACATTATTAA GCCGTATTGC AGAAAACCTA CCCAAACAGC    300

        TTGCTGTTAT AAGCCCTGAG AAGTATGACA TAAAATGTGC TGTATCTGAA GCGGCAATAA    360

        TTTTGAATTC ATGTGTGGAA CCCAAAATGC AAGTCACTAT CACACTGACA TCTCCAATTA    420

        TTCGAGAAGA GAACATGAGG GAAGGAGATG TAACCTCGGG TATGGTGAAA GACCCACCGG    480

        ACGTCTTGGA CAGGCAAAAA TGCCTTGACG CTCTGGCTGC TCTACGCCAC GCTAAGTGGT    540

        TCCAGGCTAG AGCTAATGGT CTGCAGTCCT GTGTGATTAT CATACGCATT CTTCGAGACC    600

        TCTGTCAGCG AGTTCCAACT TGGTCTGATT TTCCAAGCTG GGCTATGGAG TTACTAGTAG    660

        AGAAAGCAAT CAGCAGTGCT TCTAGCCCTC AGAGCCCTGG GGATGCACTG AGAAGAGTTT    720

        TTGAATGCAT TTCTTCAGGG ATTATTCTTA AAGGTAGTCC TGGACTTCTG GATCCTTGTG    780

        AAAAGGATCC CTTTGATACC TTGGCAACAA TGACTGACCA GCAGCGTGAA GACATCACAT    840

        CCAGTGCACA GTTTGCATTG AGACTCCTTG CATTCCGCCA GATACACAAA GTTCTAGGCA    900

        TGGATCCATT ACCGCAAATG AGCCAACGTT TTAACATCCA CAACAACAGG AAACGAAGAA    960

        GAGATAGTGA TGGAGTTGAT GGATTTGAAG CTGAGGGGAA AAAAGACAAA AAAGATTATG    1020

        ATAACTTTTA AAAAGTGTCT GTAAATCTTC AGTGTTAAAA AAACAGATGC CCATTTGTTG    1080

        GCTGTTTTTC ATTCATAATA ATGTCTACAT TGAAAAATTT ATCAAGAATT TAAAGGATTT    1140

        CATGGAAGAA CCAAGTTTTT CTATGATATT AAAAAATGTA CAGTGTTAGG TATTATTTGA    1200

        ATGGAAAGAC ACCCAAAAAA AAAAATGTGC TCCGACTAGG GGGAAAACAG TAGTTCCGAT    1260
```

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TTTTTCCCAT TATTTTTATT TTATTTTCTG GTTGCCCTAG CTTCCCCCCC TATTTTTGTG     1320

TCTTTTATTA ACTAGTGCAT TGTCTTATTA AATCTTCACT GTATTTAATG CAGGATGTGT     1380

GCTTCAGTTG CTCTGTGTAT TTTGATATTT TAATTTAGAG GTTTTGTTTG CTTTTTGACA     1440

CTAGTTGTAA GTTACTTTGT TATAGATGGT ATCCTTTACC CCTTCTTAAT ATTTTACAGC     1500

AGTACGTTTT TTTGTAACGT GAGACTGCAG AGTTTGTTTT TCTATATGTG AAGGATTACA     1560

ACACAAAAAG TTATCCTGCC ATTCGAGTGC TCAGAACTGA ATGTTTCTGC AGATCTTGTG     1620

GCATTTGTCT CTAGTGTGAT ATATAAAGGT GTAATTAAGA CAGAGTTCTG TTAATCTAAT     1680

CAAGTTTGCT GTTAGTTGTG CATTAGCAGT ATAAAAGCTA ATATATACTA TATGGTCTTG     1740

CAACAGTTTT AAAGCCTCTG CATAATTGAT AATAAAAATG CATGACATTC TTGTTTTTAA     1800

TAGACTTTTA AAATCATAAT TTTAGGTTTA ACACGTAGAT CTTTGTACAG TTGACTTTTT     1860

GACATAGCAA GGCCAAAAAT AACTTTCTGA ATATTTTTTT CTTGTGTATA AGTGGAAAGG     1920

GCATTTTTCA CATATAAGTG GGCTAACCAA TATTTTCAAA AGAACTTCAT CATTGTACAA     1980

CTAACAACAG TAACTAGCCC TTAATTATGG TGACAGTTCC TTATTGGTGT GTGTGAGATT     2040

ACTCTAGCAA CTATTACAGT ATAACACAGA TGATCTTCTC CACACACCCC ATCACCCAGA     2100

TAATTTACAG TTCTGTTAAC AGTGAGGTTG ATAAAGTATT ACTGATAAAA AATTATCTAA     2160

GGAAAAAAAC AGAAAATTAT TTGGTGTGGC CATCTTACCT GCTTATGTCT CCTACACAAA     2220

GCTAAATATT CTAGCAGTGA TGTAATGAAA AATTACATCT TACTGTTGAT ATATGTATGC     2280

TCTGGTACAC AGATGTCATT TTGTTGTCAC AGCACTACAG TGAAATACAC AAAAAATGAA     2340

ATTCATATAA TGACTTAAAT GTATTATATG TTAGAATTGA CAACATAAAC TACTTTTGCT     2400

TTGAAATGAT GTATGCTTCA GTAAAATCAT ATTCAAATTT AAAAAAAAAA AAAAAAAAAA     2460

CTCGA                                                               2465
```

(2) INFORMATION FOR SEQ ID NO: 207:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1480 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

```
GAATTCGGCA CGAGCTCAAG CTGGCAGGTG GTCGGGGGAG CGGCCGGAGA GGAGCTGCCG      60

GGAGTTCGTG CCCTGCAGGA CATGACACCA GTGGCATATC ACGGCCATGG GGTCTCAGCA     120

TTCCGCTGCT GCTCGCCCCT CCTCCTGCAG GCGAAAGCAA GAAGATGACA GGGACGGTTT     180
```

```
GCTGGCTGAA CGAGAGCAGG AAGAAGCCAT TGCTCAGTTC CCATATGTGG AATTCACCGG      240

GAGAGATAGC ATCACCTGTC TCACGTGCCA GGGGACAGGC TACATTCCAA CAGAGCAAGT      300

AAATGAGTTG GTGGCTTTGA TCCCACACAG TGATCAGAGA TTGCGCCCTC AGCGAACTAA      360

GCAATATGTC CTCCTGTCCA TCCTGCTTTG TCTCCTGGCA TCTGGTTTGG TGGTTTTCTT      420

CCTGTTTCCG CATTCAGTCC TTGTGGATGA TGACGGCATC AAAGTGGTGA AGTCACATT      480

TAATAAGCAA GACTCCCTTG TAATTCTCAC CATCATGGCC ACCCTGAAAA TCAGGAACTC      540

CAACTTCTAC ACGGTGGCAG TGACCAGCCT GTCCAGCCAG ATTCAGTACA TGAACACAGT      600

GGTGAATTTT ACCGGGAAGG CCGAGATGGG AGGACCGTTT TCCTATGTGT ACTTCTTCTG      660

CACGGTACCT GAGATCCTGG TGCACAACAT AGTGATCTTC ATGCGAACTT CAGTGAAGAT      720

TTCATACATT GGCCTCATGA CCCAGAGCTC CTTGGAGACA CATCACTATG TGGATTGTGG      780

AGGAAATTCC ACAGCTATTT AACAACTGCT ATTGGTTCTT CCACACAGCG CCTGTAGAAG      840

AGAGCACAGC ATATGTTCCC AAGGCCTGAG TTCTGGACCT ACCCCCACGT GGTGTAAGCA      900

GAGGAGGAAT TGGTTCACTT AACTCCCAGC AAACATCCTC CTGCCACTTA GGAGGAAACA      960

CCTCCCTATG GTACCATTTA TGTTTCTCAG AACCAGCAGA ATCAGTGCCT AGCCTGTGCC     1020

CAGCAAATAG TTGGCACTCA ATAAAGATTT GCAGAATTTA ATACAGATCT TTTCAGCTGT     1080

TCTTAGGGCA TTATAAATGG AAATCATAAC GTGGTTCTAG GTTATCAAAC CATGGAGTGA     1140

TGTGGAGCTA GGATTGTGAG TGACCTGCAG GCCATTATCA GTGCCTCATC TGTGCAGAAG     1200

TCGCAGCAGA GAGGGACCAT CCAAATACCT AAGAGAAAAC AGACCTAGTC AGGATATGAA     1260

TTTGTTTCAG CTGTTCCCAA AGGCCTGGGA GCTTTTTGAA AAGAAAGAAA AAAGTGTGTT     1320

GGCTTTTTTT TTTTTTAGAA AGTTAGAATT GTTTTTACCA AGAGTCTATG TGGGGCTTGA     1380

TTCACCCTTC ATCCATTGGC TGGAACATGG ATTGGGGATT TGATAGAAAA ATAAACCCTG     1440

CTTTTGATTC AAAAAAAAAA AAAAAWAAA AAAAACTCGA                           1480
```

(2) INFORMATION FOR SEQ ID NO: 208:

    (i) SEQUENCE CHARACTERISTICS:
       (A) LENGTH: 872 base pairs
       (B) TYPE: nucleic acid
       (C) STRANDEDNESS: double
       (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

```
CAGTATTTCC CTCAGTACTG TAAGCAAAAG TGGTATGTTT TTCTTTCTTT ATGTCTACTC       60
```

461

```
      TGTCCTCTGT GGCCTTCTGG TGTACCCCTC TCTTCCTAGC CATTCAGTCT CTCTAGTCAC      120

      CTCCCTAGTA GCTAGTGCTC TCTAAGTTTT TATTTAATTA GAACAACTCC ATTTCCATTT      180

 5    CAAGGTAGGT CAATGGGGGG AAAAGCCTCA TGATTTAAAC TGAAGTTAAC AACACAGCTT      240

      TTAAAATGAA AACTCATACT CCAACTTCTA AAGTATATTT GAGCTGATTT GTTTCCAAAA      300

      CAAAGATATG CTGTACCTAA AACTGCTAAA ACAAAAATAT AAAGACAAGG ACTAGGTGAT      360

10    TAAGGGGAGA GAAAAATCAT YTCTTTTCCA GGAAACCTTT GCTAAAATAA GCAAAACTTG      420

      ANTCTATGCT TCATGGAAAC TGACACAAAG AAAAGAAACT GATGGATTGC ACAGGCCTTG      480

15    TTATAGAAAT AGATCTATAA AAAGATCTGT CCACAGGAAA TATACACCTT CTCCTGGTTC      540

      TGAACTTCAA TGGGGATTTG TCACCTAGGT CTCCATCTAT AGGAATACCT TCACATACCT      600

      ATCTATTCAT GCACATATTC TGAAAACAGG TACATACAAA ATTACAACAA AGGAAAAAAA      660

20    TTCTATTGAA CACTTAAAAA TAGAAACAGG CCAGGCACGG TGGCTCATGC TGTAATCCCA      720

      ACAATTTGGG AGGCTGAGGC TGGTGGATCA CCTGAGGTCA GGAGTGTGAG ACCAGCTTGG      780

25    CCAACATGGT GAAACCCCGT CACTACTAAA AATACAAAAA AAATTAGCCT GTGTGGTGGC      840

      ACACTCNTAC AATCCNGGCT GACTCGGGAA AN                                    872
```

30

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      (2) INFORMATION FOR SEQ ID NO: 209:

              (i) SEQUENCE CHARACTERISTICS:
35                    (A) LENGTH: 1779 base pairs
                      (B) TYPE: nucleic acid
                      (C) STRANDEDNESS: double
                      (D) TOPOLOGY: linear

40            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

      AATTGCCAAG ACTGCACAAA ATTACAGTGC TAATGTATAT GGTTGCAGTT CACATAAAGA       60

      CAAAAGCATC TGTTATGAAA TGAGTAGTAA TATTGGGTGG TTGATTTGTT CTTAGCAGAC      120

45    TTGGCTTCAT WTTGGTCTTG AGATAAAATG GCCAGCATAA ATGCTGTTTA TATTCACGTT      180

      TTCCTAGGTG TGTGTGTGCA GGCCACAGCA GCATGCCCTT GGTGTAGTCA GTGCCGAAAS      240

50    GGGTCTGTTC CTTCTTGAGC CTGCCTGCAG GGATGGTCTC CTTTTAAAGC AGGTTGTGTG      300

      CAGCATTCAG TACACTGAAG GTAAGCTAAA CCATCAACAT CTCTGGTGTT TTAAGATGTT      360

      ATTTTATTGG AACAACTGAC AAATGAGGGA TGTTAGCTTT GTGGCAGAAT CCCTGCATG      420

55    TGTGATAACT GATCTTGTTT TATTTTTTGG CATTGCAACT GTGGCATAGT TACAATTTCT      480

      GTTTGKTCAT CACATTTAAA ATTGGRAGAG AACGCGCTTG AKGGATAGAG CGCCTTCAGK      540

60    GTACTGTTTC TTATTAACTT TACTTTTTTT AAATCAACTT GCTATAGACT TTATATACAT      600
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TTTGTTAAAT ATAGTTCCTA GTGACATAGA AACGATGCGT AGTTTTCATT TACTAATTAC        660

AAATGTTGAG GCCTAATTCT GAAAGTCCTC ATATTTAAAG GCTAGACAAC GTAATGAAAT        720

TTTTAACTAT TTGTATGTCA TTTTGAAAGT GTACTGCTTT ATGGTAAAAG TGTTTTTCAT        780

TTGTTCATTG TTTTCATTAT TTGTGATCAT GTTGTCTTTC AATACAGGCA TAAACCTTCC        840

ACTCTTGAAC AAAGCAGCTG CTTTTTAAAA GCGGTAATTG CTTCTTTACC TTTTATTTCT        900

TTTGTAAATG AAGCTTTTCT TTAAGAATGT GACTTTAAAG TGTTGTCTAT TGCATAAAAC        960

AGTTGACACT CACTTATTGT AAAGTGAAGA TTGTTCTACT GCATGTGAAG TGGACCATGC       1020

AGATTTCTGT ATGTTCTCAG TATGCATCAC TAGATAATAA AGTCTTTTGT GAACAAGGCA       1080

TTTGTAGCCA TTTTTAAAAG TTTTTGTCTT CAGTGCTGGT AAGTCAGGTA AACCATAAAT       1140

AGTTAAAAGC AACCTTTTGT TTTTTTCCTG AAAGTTTTTA ATTGAAAGTA TTATTAGTTA       1200

AAGATGTAAA CCTAGCCAAA ATTACCAGTT TATTAATAAT TAGGATCCTA ATTATTTCAA       1260

AAAATCCTAC AAATATTGTC AGCTTTCAGT GTAGTGAGAT TATTCCTGTA GGTTATGGGG       1320

TATAATTCAG GATTTAACTA ATGTTTCTGC TATTTTCTCA CTTTTCCTTT TGATGGTGCG       1380

GAAAGAGAAA AAGGAAAACG GGGCACAGGC CATTCGACGC CTTCTCCAAG GGGTCTGATT       1440

TGCTGAGACA CCAGCTTCAC CTTCTTAACA AGGCACCTAA TTACAACAAG CATGCACATT       1500

TTGGTGCATT CAAGAATGGA AAATCAGAAT AGCAGCATTG ATTCTTCTGG TGCAGCTCAG       1560

TGGAAGATGA TGACAACCAG AAGACATGAG CTAAGGGTAA GGGACTGTTC TGAAGAACCT       1620

TTCCATTTAG TGATCAAGAT ATGGAAGCTG ATTTCTGAAA ATGCTCAGTG TGTACTCTAA       1680

TTATTTATGG TACCATTTGA ATTGTAACTT GCATTTTAGC AGTGCATGTT TCTAATTGAC       1740

TTACTGGGAA ACTGAATAAA ATATGCCTCT TATTATCAA                             1779
```

(2) INFORMATION FOR SEQ ID NO: 210:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 2110 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

```
GCGGCCGCTG CAGCCCGGAG CTGAGCTAGC CGTCCGAGCC GAGCCGTCCG AGCCGGGGAA         60

GCCGGCGCGT GCTGCCGCTC GTGGCGGCCA GAGGAGAGGA GAGGCAGCAG CATGGCGAGT        120

GTCCTGTCCC GACGCCTTGG AAAGCGGTCC CTCCTGGGAG CCCGGGTGTT GGGACCCAGT        180
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   GCCTCGGAGG GGCCTCGGCT GCCCCACCCT CGGAGCCACT GCTAGAAGGG GCCGCTCCCC    240

   AGCCTTTCAC CACCTCTGAT GACACCCCCT GCCAGGAGCA GCCCAAGGAA GTCCTTAAGG    300

5  CTCCCAGCAC CTCGGGCCTT CAGCAGGTGG CCTTTMAGCC TGGGCAGAAG GTTTATGTGT    360

   GGTACGGGGG TCAAGAGTGC ACAGGACTGG TGGWGCAGCA CAGCTGGATG GAGGGTCAGG    420

   TGACCGTCTG GCTGCTGGAG CAGAAGCTGC AGGTCTGCTG CAGGGTGGAG GAGGTGTGGC    480

10 TGGCAGAGCT GCAGGGCCCC TGTCCCCAGG CACCACCCCT GGAGCCCGGA GCCCAGGCCC    540

   TGGCCTACAG GCCCGTCTCC AGGAACATCG ATGTCCCAAA GAGGAAGTCG GACGCATGGA    600

15 AATGGATGAG ATGATGGCGG CCATGGTGCT GACGTCCCTG TCCTGCAGCC CTGTTGTACA    660

   GAGTCCTCCC GGGACCGAGG CCAACTTCTC TGCTTCCCGT GCGGCCTGCG ACCCATGGAA    720

   GGAGAGTGGT GACATCTCGG ACAGCGGCAN CAGCACTACC AGCGGTCACT GGAGTGGGAG    780

20 CAGTGGTGTC TCCACCCCCT CGCCCCCCCA CCCCCAGGCC AGCCCCAAGT ATTTGGGGGA    840

   TGCTTTTGGT TCTCCCCAAA CTGATCATGG CTTTGAGACC GATCCTGACC CTTTCCTGCT    900

25 GGACGAACCA GCTCCACGAA AAAGAAAGAA CTCTGTGAAG GTGATGTACA AGTGCCTGTG    960

   GCCAAACTGT GGCAAAGTTC TGCGCTCCAT TGTGGGCATC AAACGACACG TCAAAGCCCT    1020

   CCATCTGGGG GACACAGTGG ACTCTGATCA GTTCAAGCGG GAGGAGGATT TCTACTACAC    1080

30 AGAGGTGCAG CTGAAGGAGG AATCTGCTGC TGCTGCTGCT GCTGCTGCCG CAGACCCCCA    1140

   GTCCCTGGGA CTCCCACCTC CGAGCCAGCT CCCACCCCCA GCATGACTGG CCTGCCTCTG    1200

35 TCTGCTCTTC CACCACCTCT GCACAAAGCC CAGTCCTCCG GCCCAGAACA TCCTGGCCCG    1260

   GAGTCCTCCC TGCCCTCAGG GGCTCTCAGC AAGTCAGCTC CTGGGTCCTT CTGGCACATT    1320

   CAGGCAGATC ATGCATACCA GGCTCTGCCA TCCTTCCAGA TCCCAGTCTC ACCACACATC    1380

40 TACACCAGTG TCAGCTGGGC TGCTGCCCCC TCCGCCGCCT GCTCTCTMTC TCCGGTCCGG    1440

   AGCCGGTCGC TAAGCTTCAG CGAAGCCCCA GCAGCCAGCA CCTGCGATGA AATCTCATCT    1500

45 GATCGTCACT TCTCCACCCC GGGCCCAGAG TGGTGCCAGG AAAGCCCGAG GGGAGGCTAA    1560

   GAAGTGCCGC AAGTGTATGG CATCGAGCAC CGGGACCAGT GGTGCACGGC CTGCCGGTGG    1620

   AAGAAGGCCT GCCAGCGCTT TCTGGACTGA GCTGTGCTGC AGGTTCTACT CTGTTCCTGG    1680

50 CCCTGCCGGC AGCCACTGAC AAGAGGCCAG TGTGTCACCA GCCCTCAGCA GAAACCGAAA    1740

   GAGAAAGAAC GGAAACACGG AGTTTGGGCT CTGTTGGCTA AGGTGTAACA CTTAAAGCAA    1800

55 TTTTCTCCCA TTGTGCGAAC ATTTTATTTT TTAAAAAAAA GAAACAAAAA TATTTTTCCC    1860

   CCTAAAATAG GAGAGAGCCA AAACTGACCA AGGCTATTCA GCAGTGAACC AGTGACCAAA    1920

   GAATTAATTA CCCTCCGTTT CCCACATCCC CACTCTCTAG GGGATTAGCT TGTGCGTGTC    1980

60
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464

AAAAGAAGGA ACAGCTCGTT CTGCTTCCTG CTGAGTCGGT GAATTCTTTG CTTTCTAAAC   2040

TCTTCCAGAA AGGACTGTGA GCAAGATGAA TTTACTTTTC TTAAAAAAAA AAAAAAAAAA   2100

5   AAAAACTCGA   2110

10   (2) INFORMATION FOR SEQ ID NO: 211:

          (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 938 base pairs
                   (B) TYPE: nucleic acid
15   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

20   GGCACAGGAA AAAAAGAAA AAAGAAAAAA GAAAAAAGTT TTTGTACCCA CAGATTAGCA   60

     TTTTCTTGAT GTTTGAAAAA AGTTTAAGCT ATGTCCTAAT TTAAAAATGA GCACAAACTA   120

     CTTAACAGAT GTCTGTTCCC TCTTCTCTTA CTTAAATTAT CTTTATTTTC ACCATCACCT   180

25   CCCAGTGCCG AACACCTGAN CTCTGTGTTT TGTGGTTGGA TCCTGGGTTG CCAAGTTCCT   240

     ATTTGGTCAG TCCCTGGCCT GTGGGGCGGT CTCAGGAAGT GGCATGCTCT TCAMGRAGGA   300

30   TCGTTCATYT CCAGTATAAC CAWTTTGTTA ATAATAGTTG ATAATTCCCA GCTTTTACCA   360

     GATGARTTTT GACTTATTTT TCCTCCTTTG ACCTGTTCAA AGCTAACATA TCTCGGTCAG   420

     TTCGGAGAGG GTGGGGGATT TGAGAATGTG AGGAGGAGTG GGGTTAGAAT GGGTTTGCCT   480

35   ATCTGGGCAA GGAAAGAGTT CCTAGTCGAT TGGGCACAAT GACAAAATGA TTCCATGGAT   540

     AGAATCGTCC CATGTTGCTG GAACACCTCA CGTGTTGTGA ACGCCTTAAA TTCCTGCCAT   600

40   CCCTTCTCTG ATTCCCCACC TCCCTGTAGT TTCCACAGGA TTTATCTCTC TGTACCCCCG   660

     TCCTCCAACT CTACTCTGTC AGCCTCTCCT CCATCCCTTA CTTCCCTTCT AAATTCCAGG   720

     AGATGACCTC ACTTTGCAAA GCAAATTGGA GCCACCAAAT TGTAGCTCTC CTCGGTGGAA   780

45   ACTGCATCTG TGCTCATCCC TGCACCTTCT TGCAGAAAGC CGCCCCCTCA GGCCAAGATG   840

     AGTGCCTGGC CCCCATGGGA GACTCAGACA CTTTGACCCC TTGTGACTTC AGCATCTCCC   900

50   TCTTTAAAGA TTCTCTCCCA ACATTCAGTC GTGCTCGA   938

55   (2) INFORMATION FOR SEQ ID NO: 212:

          (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 1551 base pairs
                   (B) TYPE: nucleic acid
60   (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

```
5    AGGCTGGACT AAGCATAGAG AACCAGGAGA GAAAGAAAGA TTTAAGAGAC TGAGTAATAT      60

     TTTTTGACAG ATCATTTAAG AAACTGAGTA ATTTTTTTTT CTCCAAAAG GGCATGGGTT       120

     TTTTTTTTGT TTTGTTTTTT CTCTATTTGG CACTTTCTAG GGATTGGTCT ATAAATTTTT . 180
10
     TGAAAGATCA TAGGATAAAT TTCTTTGTAG CAACTTCCTA TTTTAGTGTT TATGTTAGGG      240

     GARCCCCARG TGTCCCTGCT GATACGCCAT TAGGGCCACT TCTCAGCCTC TGGCTACATC      300

     ATAATGCTTT TTTTTCTATC TTGCCAAAGT TTCCMGAAAA TTKAKGTTTT CTAATTTTAA      360
15
     AAAAATTGGT TGTGGAGATG GGATGGGACC TCTTTATAAG CCCTGAAAAT AAGTGATTTN      420

     TTTTAAGTGC TATTCTGCTA TAAACCTGAT TCTCACTTTT TTCTGTAGAC AACAGTTTTT      480

     TATAATATAT CTATTTTGTG TGGACATTAT TTCCTTTTAA CCAATACTGA AATTCCATAG      540
20
     TGTAWACTTT CTCCACATTT TCTTTGATTA ATACTTYCTT AAAATAGACA CTTGGATTGG      600

     CACCAGCTGT CACCAATAAA GCTGCCCTGA ACATTGTCAA TCAATCCTGT TAACCAATTT      660
25
     GAGAATTTTT CTGGAATGCT TAGTTAGGGA TGAAATTGCT GGGTTATAGG TATGAGTATG      720

     CTTGATATAC TTTTCTCCAG AATGTCTACA CCTGTGTGTA CACCACATCT CCAGAGATAG      780
30
     GGGAATCTTA TGTCCCTGCT AACTGCTCTC GTTATTTAAT TTTCTGACAT TTGCCGCCGC      840

     CGCCGCCCCC TGCCCCCAAC ACACACATGG TATAAAGTGG TAGTTTCTTG TTTTAAATTG      900
35
     AACTTTTGAA TGATTTGAAT TTGGGCATTT CTTTGTATCC TGAGTTATTT TGGTTTCCCG      960

     TTATGTGAAT ATCCTTTTCC TATGCTTTAA CTACTTTTCT AATTTGTCCC TTTTTTNGGT     1020

     TATCAAATTC CAGGCCATTG TCTATTCCAT CGTCACTTTT GGGTATTGGA AACATCTTTC     1080
40
     CATTCTGTAG CCTGTCTGTT GAACATAAAT CTTGATTTTT ATGTAATCAG ATTTTTCTCC     1140

     TTACGGTTAT GTTCTTGGAA TTTTATTTAA GAAATCTTTT TCTATCCTGA GACCACAAAA     1200
45
     ATGTCCCCAC CATTTTCTTC TGTTTCATAG TTTTGCCTTG TATGTTTAAT CCTTTAAGGC     1260

     ATGTGTAGTT CATTTTATAT GGTGTGAAAT AGTTCTTATT CATTTATTCA ACACATATTG     1320
50
     GTGGAGTGCC TGCTGATGGT AGTACTCTTC AGAGTACTTT GTATATATTT GTGAACACAT     1380

     ATTCTTGCCC TGGAAGCTTA TGTTGTCNTT CAAGGTAGAT CCNTACTCGG TTTCCACCTG     1440

     TTTTCTTCAG CCCTCAGGAT GAATTCCACA ATTTTACACA TAGCACCAGT TAAGGAATAG     1500
55
     GCTTTATTGG AGAAAAGGAA GGCTTATTAG ACCAGCATCA GCAAAAAAAA A              1551
```

60   (2) INFORMATION FOR SEQ ID NO: 213:

466

(i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 997 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

```
AGAGAGTCCT CAACAGAACC TAATCATGCT GGCACCCTAA TCTCATACTT CTAGCCTCCA      60

GAACTGAGAG AACATAAACT CCAGTTGTTT AAGCTACCCA GACTATGGTA TTTGTTATTA     120

TAGCCCAAGC TAAGTCAGGT GGAAAGGCAG AAATATTTTG AGAAGATCA TTTCTACAAA     180

AACAGAGTTG TTCTAAATGA AATGGCCAGA TATTTCATCT TCTTCATACT AGTATTTATG     240

AAAGTTTCAT TAAACACCAC TTGGCCAGCA CCCAGGCCTG CCACCCTCAG AACGGCAAAC     300

AAAAGCAAAT GATTTGAGGA ACAAAAGAGT GGACACAGAG CTTCTCAGAA GATGGCTCCA     360

TCTTCTGAGA TGATCTTCTG AGATCATCAA TTTTCTGCAC CTGATGTCCT ACTCCAATTG     420

TAGTAGATAA GAGCAAAGAC ACTTCCTGAT CCTGTGGAAA ATGCTGGAGC CCTGCTGATG     480

GAGAGGCTGA CACTGGGACC AACAGAAGGC CGGACATTTA TTTGTTGCAG CCCTTCTGCA     540

CCTGGGCCCT CTTCAGGCCT TGTACCTTGC ACTCCCCATG CCACTGTAGC ACCTGGTAAG     600

CTGAAGTTAG GTATTTGAAG AGATAATTTG CCCCCAACAA AGAATTACTT AAAAGAAAAA     660

GGAAACCACT AAATTCCACT TGACAAACCA GTTTGTTCAG TTTTGACTTT TGCAAATTTG     720

AAACTTTCTC TTTGGCACCA TATGATTCTG TTACATTAGG GTTCATCAAT GCTAAGATAC     780

ACAGCTAGGT CTACCAGCTG CCAGTGGTCA AGAATGAAAG AACCTCTCAG AGAGAGATCA     840

GTTTCTAATA ACCTAACAGT TTTCCTTGGS TATTACMAAA AAAAAAAAAA TTAGAATAAA     900

ATGTCAGTGC CATGCAGGCA AGTACAGATA TGGAAATGAA AGCTTTGTCT ACAACTGCAA     960

GATTTGTTTG TTAATAAAAT TGATTGGGAT CACTCGA                             997
```

(2) INFORMATION FOR SEQ ID NO: 214:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1496 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

```
GAATTCGGCA CGAGTGACCA CAGATATCTT TGGCTTTCAG CCTCACCACA ATGCTGTCCA      60

CTATGTTTTT TTTAATCGAT TGACATCTCA TGAATCCACA AATTAGCCG CTTTTCCATC     120
```

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TTTTCCATCT TTGTCATAGC TTCATCACGC ACGATGGAGG TCACTTCAGC ACTATCCGGA     180

GCGGCCTCAC GGACAGATCR GTGAATTTCC TTTTCCTTTT TCTTGATGTA CCGGATTGTC     240

GACTCGTTAA CATTGAGCTC ATGGCCAACA GCACTGTAAC TCATGCCTGA TTGGAGCTTA     300

TCCAACACGC GGAMTTTCTC CGTAAGGSAM ATCAMGGTCT TCTTTCGCTT AGGAACACTG     360

GGCARARCTT AARCACTACG CTTGGGGGCC ATTTTAGAAA GCAAAACCAC CCACAAAAAG   · 420

CAGAAAAAAA AGTGTCAGTA AACAGACTGN NGANAGGACT CTTTGTTTAC AGCACAGGAG     480

CTGCGACTAG AAGGCGGCGC TTCTCCCCAG TTCAAACTTC AGCTGGGAAC CTTACCTCCG     540

CCAACTCCAA ATTTTCACCC TCTGCGCATG CCCGGGAAAS AAACCCCCAG AACAGTACCG     600

TGATGATTGA TTTTAGGGTT ACAAATACAT TTTAGCAAGT AAGTGAATTT GGCATTACGA     660

ATTAATGATT AATGAAGGTC ACCTGTATTT CCATAGATAT GTAATTTTAT TTAAGCAGGT     720

TTATTATATT AAGGCGGSGA GGCAGCGCCG AAGACTACAA GTTCCAGCAT GCACCGCGTC     780

CGGGCGGGTT CGGGCTCCCA GCGAGGGCTT CAGGGACGCC AGCCCGGAGG CATCGGCCGG     840

AAGTGTCGTA GGGCAACCAC GTAGTACTCT CTGCGCATGT GCAAAGCGCT GTCGGGGGCC     900

GCCCTAGCTG CCGTCGCCGC CGCCGGGGCT CTATGGTCTC TCCCTAGAGC TTTGCCGTTG     960

GAGGCGGCTG CTGCGGTCTT GTGAGTTTGA CCAGCGTCGA GCGGCAGCAA CATGGAGGAA    1020

TTCGACTCCG AAGACTTCTC TACGTCGGAG GAGGACGAGG ACTACGTGCC GTCGGGTGAG    1080

CGATTCCGCC TGAGGCGAGA AGCGAATTGC CCCGCCCCAC GCCTCACGTG AGGCGCGCTC    1140

TGCCCCCGCG GGCGTCTGCC CTGTGGCCCA GGTGGTCCAG GGGGGCTCCT GTTCTCGAGC    1200

GTCCGCTCCC TCAGGCCCCT CATCCTCGGC CGCTCCGGCC CGAGGCGTGT GCGCGTGGCG    1260

GTTCTGTGCT CCCCTCCCGT TGGGCAGCTC CGGCCGCCGC CCCCTCTTGC AGCGCGGGAA    1320

CGGCACATGG ACACGGCCCC TTGTCGCTAG GGACGCTCGT CGGTCAGCCC CGAACGACAA    1380

CGCTGCTTCA GAAGTCGGGG CGGCAGTTCG AGCCTTGGAA GTTTTTTTCA GCCCTGGCCC    1440

GAGAGAGCTG CTGGCCAACA ACCCGTCCAA GATAGAGCTG TCCGNTCTCC GNCTGG       1496
```

(2) INFORMATION FOR SEQ ID NO: 215:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1308 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

```
TTGGCANCNG GGAGAGGGAA AGAGGAGGAA ATGGGGTTTG AGGACCATGG CTTACCTTTC       60
```

```
CTGCCTTTGA CCCATCACAC CCCATTTCCT CCTCTTTCCC TCTCCCCGCT GCCAAAAAAA      120

AAAAAAAAGG AAACGTTTAT CATGAATCAA CAGGGTTTCA GTCCTTATCA AAGAGAGATG      180

TGGAAAGAGC TAAAGAAACC ACCCTTTGTT CCCAACTCCA CTTTACCCAT ATTTTATGCA      240

ACACAAACAC TGTCCTTTTG GGTCCCTTTC TTACAGATGG ACCTCTTGAG AAGAATTATC      300

GTATTCCACG TTTTTAGCCC TCAGGTTACC AAGATAAATA TATGTATATA TAACCTTTAT      360

TATTGCTATA TCTTTGTGGA TAATACATTC AGGTGGTGCT GGGTGATTTA TTATAATCTG      420

AACCTAGGTA TATCCTTTGG TCTTCCACAG TCATGTTGAG GTGGGCTCCC TGGTATGGTA      480

AAAAGCCAGG TATAATGTAA CTTCACCCCA GCCTTTGTAC TAAGCTCTTG ATAGTGGATA      540

TACTCTTTTA AGTTTAGCCC CAATATAGGG TAATGGAAAT TTCCTGCCCT CTGGGTTCCC      600

CATTTTTACT ATTAAGAAGA CCAGTGATAA TTTAATAATG CCACCAACTC TGGCTTAGTT      660

AAGTGAGAGT GTGAACTGTG TGGCAAGAGA GCCTCACACC TCACTAGGTG CAGAGAGCCC      720

AGGCCTTATG TTAAAATCAT GCACTTGAAA AGCAAACCTT AATCTGCAAA GACAGCAGCA      780

AGCATTATAC GGTCATCTTG AATGATCCCT TTGAAATTTT TTTTTTGTTT GTTTGTTTAA      840

ATCAAGCCTG AGGCTGGTGA ACAGTAGCTA CACACCCATA TTGTGTGTTC TGTGAATGCT      900

AGCTCTCTTG AATTTGGATA TTGGTTATTT TTTATAGAGT GTAAACCAAG TTTTATATTC      960

TGCAATGCGA ACAGGTACCT ATCTGTTTCT AAATAAAACT GTTTACATTC ATTATGGGGT     1020

ATGTATGACC TTCATTTTCC AAGAAATAGA ACTCTAGCTT AGAATTATGG ATGCTCTAAA     1080

ATGTCAGAAT GGGAACTCTC CTCGAAGTTC TCCCAAACTC AGAGACAGCA CTGCCTTCTC     1140

CTAAATGATT ATTCTTTTCT CCCTGTTTTC TGGTATTTTC TAGGCATCCT TCTCACCACA     1200

GCCATAACCC TTTTTTACTT CCATTAGGCC GTATAACTGG NGGGACNGCT GGTCGGTATA     1260

TAATACTGGT WCCAACAMAG GGGTTCTGGA TGTACACMAG GTTATCTT              1308
```

(2) INFORMATION FOR SEQ ID NO: 216:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 1705 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

```
TGGCCATGGA AGCGCTAGAA GGTTTAGATT TTGAAACAGC AAAGAAGGAT TTCCTTGGAT       60

CTGGAGACCC CAAAGAAACA AAGATGCTAA TCACCAAACA GGCTGACTGG GCCAGAAATA      120
```

TCAAGGAGCC CAAAGCCGCC GTGGAGATGT ACATCTCAGC AGGAGAGCAC GTCAAGGCCA   180

TCGAGATCTG TGGTGACCAT GGCTGGGTTG ACATGTTGAT CGACATCGCC CGCAAACTGG   240

ACAAGGCTGA GCGCGAGCCC CTGCTGCTGT GCGCTACCTA CCTCAAGAAG CTGGACAGCC   300

CTGGCTATGC TGCTGAGACC TACCTGAAGA TGGGTGACCT CAAGTCCCTG GTGCAGCTGC   360

AGTGGAGACC CAGCGCTGGG ATGAGGCCTT TGCTTTGGGT GAGAAGCATC CTGAGTTTAA   .   420

GGATGACATC TACATGCCGT ATGCTCAGTG GCTAGCAGAG AACGATCGCT TTGAGGAAGC   480

CCAGAAAGCG TTCCACAAGG CTGGGCGACA GAGAGAAGCG GTCCAGGTGC TGGAGCAGCT   540

CACAAACAAT GCCGTGGCGG AGAGCAGGTT TAATGATGCT GCCTATTATT ACTGGATGCT   600

GTCCATGCAG TGCCTCGATA TAGCTCAAGA TCCTGCCCAG AAGGACACAA TGCTTGGCAA   660

GTTCTACCAC TTCCAGCGTT TGGCAGAGCT GTACCATGGT TACCATGCCA TCCATCGCCA   720

CACGGAAGAT CCGTTCAGTG TCCATCGTCC TGAAACTCTT TTCAACATCT CCAGGTTCCT   780

GCTGCACAGC CTGCCCAAGG ACACCCCCTC GGGCATCTCT AAAGTGAAAA TACTCTTCAC   840

CTTGGCCAAG CAGAGCAAGG CCCTCGGTGC CTACAGGCTG GCCCGGCACG CCTATGACAA   900

GCTGCGTGGC CTGTACATCC CTGCCAGATT CCAAAAGTCC ATTGAGCTGG GTACCCTGAC   960

CATCCGCGCC AAGCCCTTCC ACGACAGTGA GGAGTTGGTG CCCTTGTGCT ACCGCTGCTC   1020

CACCAACAAC CCGCTGCTCA ACAACCTGGG CAACGTCTGC ATCAACTGCC GCCAGCCCTT   1080

CATCTTCTCC GCCTCTTCCT ACGACGTGCT ACACCTGGTT GAGTTCTACC TGGAGGAAGG   1140

GATCACTGAT GAAGAAGCCA TCTCCCTCAT CGACCTGGAG GTGCTGAGAC CCAAGCGGGA   1200

TGACAGACAG CTAGAGATTT GCAAACAACA GCTCCCAGAT TCTTGCGGCT AGTGGGAGAC   1260

CAAGGGACTC CATCGGAGAT NAGGACCCGT TCACAGCTAA GCTRAGCTTT GAGCAAGGTG   1320

GCTCARAGTT CGTGCCAGTG GTGGTGAGCC GGCTGGTGCT GCGCTCCATG AGCCGCCGGG   1380

ATGTCCTCAT CAAGCGATGG CCCCCACCCC TGAGGTGGCA ATACTTCCGC TCACTGCTGC   1440

CTGACGCCTC CATTACCATG TGCCCCTCCT GCTTCCAGAT GTTCCATTCT GAGGACTATG   1500

AGTTGCTGGT GCTTCAGCAT GGCTGCTGCC CCTACTGCCG CAGGTGCAAG GATGACCCTG   1560

GCCCATGACC AGCATCCTGG GGACGGCCTG CACCCTCTGC CCGCCTTGGG GTCTGCTGGG   1620

CTGTGAAGGA GAATAAAGAG TTAAACTGTC AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA   1680

AAAAAAAAAA AAAAAAAAAA AAANA   1705

(2) INFORMATION FOR SEQ ID NO: 217:

        (i) SEQUENCE CHARACTERISTICS:

470

```
        (A) LENGTH: 999 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

AGCAAATCAC CTTAACGATC TGGAATGAAA CTGTGACCAG TGCCGCCCTG GGTGGTTCTG      60

GAGAGACTGC CGTCTTCTTG TTTGGCCATA GGTGCTGGGG CCCCGGCTTC AGTCACTGTC     120

TCAGACAGKA GTCCCGATAA GCAGATCACC AGTCCTCCAC TGTCCTTCCT GTCGGCCTTG     180

CTGCATGAGA AGATAGCTGC TTCCTCCCTC TTTTCCTACA CTGTAAATTA TTGTTTTACA     240

ATTGAGTGYC TTAATAATAG TYTACAAATA CTATGTATTT ATGCAAAACT GTTAAAGTTC     300

TCATCTGTTA TGATTGGATA CTTGGTCTTG TCAGTAGTGG TCAGCATTGG GTTGTGAGCT     360

TGTCCTACTC CATACGTGTT TATCCTGCTA TGCATTTTAC ATTGTGTGTT CACATCTATT     420

CCAAGGAGCC TTGCTAGAAA CAACACTGGC GGTTCCTGCA GGCCAGGCAG GCATTGGCCC     480

ATGCTGTGTC CCATAGGAGC CAATGGAAAG AACGTAGCTT GGTCTGCTAG CCAGCCGTGG     540

GGTGGCGCAG GCCAGGCAGC CTCTGCACCA GAGTCCAGCA CCTGCCCATT CCCCAGTCAC     600

ACAATCATAC TCTTCTTTCA TAGAGATTTT ATTACCACCT AGACCACCCT AGTTTTCCTC     660

TCTGTTAGTG TCCTGAGCTC TTTTGCAACA AAATGTAGGT ACAGACCAAT CCCTGTCCCT     720

TCCCCAATCA GGAGCTCCAC ACCATGAGTT GTTTGGTTTT CCAGAAGCTG CCAGTGGGTT     780

CCCGTGAATT GCGTTAAGAT ATCGATGATK TTTTTTATTG TTTTTCTTCT TGTTTTTTTA     840

AATAATATAT TTAAAGGCAG TATCTTTTGT ACTGTGAATT TGCAGTAGAA GATGCAGAAT     900

GCACTTTTTT TTTACTTCTG TTGGTGTGTA TTGTATATAG TGTGTGTGCT TCTTGTGATG     960

AAAATAAACT TTTTCTTTAT AAAAAAAAAA AAAAAAAC                            999



    (2) INFORMATION FOR SEQ ID NO: 218:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 941 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

GGCACGAGTA GCATTTCATT TAATCTGCAG GTATATTCTC CCAACAGTTT ATTGTCATGT      60

GATGTCCTCA GCCAAGATTG TRAGGCAGAG AGGAGCTGTC CCAACCTACT ATACCACCGA     120

GGCTGGAGAG ATCATATTTT TGGTATTAAA CTGGAGTCTC TCCATCCTTC ACATTGTTGA     180
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60

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   TGTCCTCTGT AGCAAACCGG AAAAGTCAGT GACAGAAGAT GCCGCTAGCG GTTTGAGCCA      240

   GAGAATGACA GCTCTGGTTT GGAGAAAAGG GCCGGATGGT GGCTCTAGAA AGCCCATCCT      300

5  TCTGCTCTTC TTTTTTCTCC CCCTTATATT GTGCTTTCAT TCATTCATTC ATTCATCAAA      360

   CATTTGTTGA GCACCTATTA TGTGTCAAGC TCTGTGCTAG CCTCTGGAAA ACCTGCCCTC      420

   ATGTAGCTCA CTGTGGAGTA GGAGAAACAA TGACTACACT ATGATAAGCA CGGGTTGTCA      480

10 GGGTCTCACA GAGCAGTGGC CCCTCATCCA GACCGATGAG GTCAAAGAAG GCATCCAGGC      540

   GAGGATGGTG TCAGAGCTAA CTGAAGAATG AGAGGGAGCT GCACCASCAG GGGTTGGAAC      600

15 TGAAGGTGGC AGTGCCTGGA GTCTTGATTC CAGCAGAGGG AGAGCAGTCT GTGAAAAGGC      660

   ACCAAGGGTG GGAGAGGGCA GAGCACATGG AGGAACTTCA GGTAGTTCTG GATGGCSCTG      720

   GGGCAAAGCT AGAGAGGTAA GAAGAATCTA CAAATGTTCC TCGAGTTACA TGAACTTCCA      780

20 TCCCAATAAA CCCATTGGAA ACGAAAAATT TAAGTCAGAA GTGCATTTAA GGCTGGTCCG      840

   AGTAGAATGA TTTTTACAAC GAATTGATCA CAACCAGTTA CAGATGTCTT TGTTCCTTCT      900

25 CCACTCCCAC TGCTTCACCT GACTAGCCTT TAAAAAAAAA A                          941
```

30   (2) INFORMATION FOR SEQ ID NO: 219:

           (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 575 base pairs
                 (B) TYPE: nucleic acid
35   (C) STRANDEDNESS: double
                 (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

```
40 TAAGTGGAAT CCCCCGGGGT TGCAGGGAAT TCGGCACGAG GCATTCTGAG AAGCTTAAGA      60

   CATACTTTGA AGACAACCCT AGGGACCTCC AGCTGCTGCG GCATGACCTA CCTTTGCACC      120

   CCGCAGTGGT GAAGCCCCAC CTGGGCCATG TTCCTGACTA CCTGGTTCCT CCTGCTCTCC      180

45 GTGGCCTGGT RCGCCCTCAC AAGAAGCGGA AGAAGCTGTC TTCCTCTTGT AGGAAGGCCA      240

   AGAGAGCAAA GTCCCAGAAC CCACTGCGCA GCTTCAAGCA CAAAGGAAAG AAATTCAGAC      300

50 CCACAGCCAA GCCCTCCTGA GGTTGTTGGG CCTCTCTGGA GCTGAGCACA TTGTGGAGCA      360

   CAGGCTTACA CCCTTCGTGG ACAGGCGAGG CTCTGGTGCT TACTGCACAG CCTGAACAGA      420

   CAGTTCTGGG GCCGGCAGTG CTGGGCCCTT TAGCTCCTTG GCACTTCCAA GCTGGCATCT      480

55 TGCCCCTTGA CAACAGAATA AAAATTTTAG CTGCCCCAAA AAAAAAAAAA AAAAAAAAA      540

   CTCGAGGGGG GGCCCGTACC CAATTCGCCC TATAA                                575
```

60

(2) INFORMATION FOR SEQ ID NO: 220:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 3018 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

```
GCCAGCCTTA CAGGTTTTAC GTGAAATGAA AGCCATTGGA ATAGAACCCT CGCTTGCAAC        60

ATATCACCAT ATTATTCGCC TGTTTGATCA ACCTGGAGAC CCTTTAAAGA GATCATCCTT       120

CATCATTTAT GATATAATGA ATGAATTAAT GGGAAAGAGA TTTTCTCCAA AGGACCCGGA       180

TGATGATAAG TTTTTTCAGT CAGCCATGAG CATATGCTCA TCTCTCAGAG ATCTAGAACT       240

TGCCTACCAA GTACATGGCC TTTTAAAAAC CGGAGACAAC TGGAAATTCA TTGGACCTGA       300

TCAACATCGT AATTTCTATT ATTCCAAGTT CTTCGATTTG ATTTGTCTAA TGGAACAAAT       360

TGATGTTACC TTGAAGTGGT ATGAGGACCT GATACCTTCA GCCTACTTTC CCCACTCCCA       420

AACAATGATA CATCTTCTCC AAGCATTGGA TGTGGCCAAT CGGCTAGAAG TGATTCCTAA       480

AATTTGGGAA AGATAGTAAA GAATATGGTC ATACTTTCCG CAGTGACCTG AGAGAAGAGA       540

TCCTGATGCT CATGGCAAGG GACAAGCACC CACCAGAGCT TCAGGTGGCA TTTGCTGACT       600

GTGCTGCTGA TATCAAATCT GCGTATGAAA GCCAACCCAT CAGACAGACT GCTCAGGATT       660

GGCCAGCCAC CTCTCTCAAC TGTATAGCTA TCCTCTTTTT AAGGGCTGGG AGAACTCAGG       720

AAGCCTGGAA AATGTTGGGG CTTTTCAGGA AGCATAATAA GATTCCTAGA AGTGAGTTGC       780

TGAATGAGCT TATGGACAGT GCAAAAGTGT CTAACAGCCC TTCCCAGGCC ATTGAAGTAG       840

TAGAGCTGGC AAGTGCCTTC AGCTTACCTA TTTGTGAGGG CCTCACCCAG AGAGTAATGA       900

GTGATTTTGC AATCAACCAG GAACAAAAGG AAGCCCTAAG TAATCTAACT GCATTGACCA       960

GTGACAGTGA TACTGACAGC AGCAGTGACA GCGACAGTGA CACCAGTGAA GGCAAATGAA      1020

AGTGGAGATT CAGGAGCAGC AATGGTCTCA CCATAGCTGC TGGAATCACA CCTGAGAACT      1080

GAGATATACC AATATTTAAC ATTGTTACAA AGAAGAAAG ATACAGATTT GGTGAATTTG       1140

TTACTGTGAG GTACAGTCAG TACACAGCTG ACTTATGTAG ATTTAAGCTG CTAATATGCT      1200

ACTTAACCAT CTATTAATGC ACCATTAAAG GCTTAGCATT TAAGTAGCAA CATTGCGGTT      1260

TTCAGACACA TGGTGAGGTC CATGGCTCTT GTCATCAGGA TAAGCCTGCA CACCTAGAGT      1320

GTCGGTGAGC TGACCTCACG ATGCTGTCCT CGTGCGATTG CCCTCTCCTG CTGCTGGACT      1380

TCTGCCTTTG TTGGCCTGAT GTGCTGCTGT GATGCTGGTC CTTCATCTTA GGTGTTCATG      1440
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473

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CAGTTCTAAC ACAGTTGGGG TTGGGTCAAT AGTTTCCCAA TTTCAGGATA TTTCGATGTC    1500

AGAAATAACG CATCTTAGGA ATGACTAAAC AAGATAATGG CAGTTTAGGC TGCACAACTG    1560

GTAAAATGAC TGTAGATAAA TGTTGTAATT AGTGTACACG TTTGTATTTT TGTTAATATA    1620

GCCGCTGCCA TAGTTTTCTA ACTTGAACAG CCATGAATGT TTCATGTCTC CCTTTTTTTT    1680

TTGTCTATAG CTGTTACCTA TTTTAGTGGT TGAAATGAGA GCTAGTGATG ACAGAAGGAT .  1740

GTGGAATGTC TTCTTGACAT CATTGTGTAT TGCTGGTAAT CAAGTTGGTA ACGACTACTT    1800

CTAGCAGCTC TTACCACTAT GACTTAAGTG GTCCTGGAAG GCAGTAAGTG GAGGTTTGCA    1860

GCATTCCTGC CTTCATGAGG GCTTCTACCA CTGACCACTT TGCACGTACC TGGCTCCCAG    1920

ATTTACTTAG GTACCCCACG AGTCGTCCAC ATAAGCAGCT TCATCTTTAC CTTGCCAGAG    1980

TTGACAATTA TGGGATACTC TAGTCTACTT ATACTTGTGT TCCCATCTGT CTGCCATCCT    2040

CTGAAGGCCA GGACCCAGTC ATACATCCTT AGAAACCAAA GTATGGTTTT TGTTTTCTCT    2100

TGGAATGTCA GGTCTTAAGG CATTTAATTG AGGGACAAAA AAAAAAAAAA GCCGATATAG    2160

TAGCTAGCTA CTTAAGCATC CATGGGTATT GCTCCATATC AAAGCAGATT TGCAGGACAG    2220

AAAGAGTAAA TTAGCCTTCA GTCTTGGTTT ACAGCTTCCA AGGAGAGCCT TGGSCACCTG    2280

AAATGTTAAC TCGGTCCCTT CCTGTCTCTA GTTCATCAGC ACCTGCAGAT GCCTGACTCT    2340

TGTTAGCCTT ACTATTCAAT ACAGTCCTTA GATTCACGGT ATGCCTCTTC CTATCCAGGC    2400

ACCTATTCTG AATCACCATG TTGCTCTGCA GCTAGAGTTG ATAGGAGAAA ATCCATTTGG    2460

GTAGATGGCC TATGAATTTG TAGTAGACTT TCAAAATGAG TGATTTGTTA GCTTGGTACT    2520

TTTAAGTTTG TGGTACAGAT CCTCCAAACC CATACTCTGA GCAATTAACT GCCTTGAACA    2580

TAGAGAAAAA TTAAGGCCTC ACAGGATGAG TCTCCATTCT CTGTAAATGC TTATTTTATC    2640

ATAGTCTTTA GCCTCTAACT ATGAGTAAAA TGTTCTCTTC GGCCGGGTGT GGTGACTCAC    2700

ACCTGTAACC TCAGCACTTT GGGAGGCAGA GGTGGGAGGA TCACTTAGGT CCAGGAGTTC    2760

GAGACTAGCC TGGGCAACAT AGTGAGACAC CGGATCTACA AAAAAATAAA AAGCCAGACT    2820

GGTGGTATGT ATCTGTGTCC CAGCTAATTG GGAGGGTGAG ATGGGAGGAT TGTTTGAGCC    2880

TAGGAGAGGG AGGTTGCAGT GAGCCGTGAT CGCACCACTG CACTCCAGCC TGGGCAACAG    2940

AGCAAGACCC TGTCTTGGAG AAACCAGAAT TTTGGAAGAG CAAATGGGGC TGAGTGCAGT    3000

GGCTCATGCC TGTAATCC                                                  3018
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(2) INFORMATION FOR SEQ ID NO: 221:

      (i) SEQUENCE CHARACTERISTICS:

474

```
              (A) LENGTH: 968 base pairs
              (B) TYPE: nucleic acid
              (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear
5
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

    GGCACGAGGG CCGCGGGACA TCCACGGGGC GCGAGTGACA CGCGGGAGGG AGAGCAGTGT      60

10  TCTGCTGGAG CCGATGCCAA AAACCATGCA TTTCTTATTC AGATTCATTG TTTTCTTTTA     120

    TCTGTGGGGC CTTTTTACTG CTCAGAGACA AAAGAAAGAG GAGAGCACCG AAGAAGTGAA     180

    AATAGAAGTT TTGCATCGTC CAGAAAACTG CTCTAAGACA AGCAAGAAGG GAGACCTACT     240

15  NAAATGCCCA TTATGACGGC TACCTGGCTA AAGACGGCTC GAAATTCTAC TGCAGCCGGA     300

    CACAAAATGA AGGCCACCCC AAATGGTTTG TTCTTGGTGT TGGGCAAGTC ATAAAAGGCC     360

    TAGACATTGC TATGACAGAT ATGTGCCCTG GAGAAAAGCG AAAAGTAGTT ATACCCCCTT     420

20  CATTTGCATA CGGAAAGGAA GGCTATGCAG AAGGCAAGAT TCCACCGGAT GCTACATTGA     480

    TTTTTGAGAT TGAACTTTAT GCTGTGACCA AAGGACCACG GAGCATTGAG ACATTTAAAC     540

25  AAATAGACAT GGACAATGAC AGGCAGCTCT CTAAAGCCGA GATAAACCTC TACTTGCAAA     600

    GGGAATTTGA AAAAGATGAG AAGCCACGTG ACAAGTCATA TCAGGATGCA GTTTTAGAAG     660

30  ATATTTTTAA GAAGAATGAC CATGATGGTG ATGGCTTCAT TTCTCCCAAG GAATACAATG     720

    TATACCAACA CGATGAACTA TAGCATATTT GTATTTCTAC TTTTTTTTTT TAGCTATTTA     780

    CTGTACTTTA TGTATWAAAC AAAGTCMCTT TTCTCCMAGT TGKATTTGCT ATTTTTCCCC     840

35  TATGAGAAGA TATTTTGATC TCCCCAATAC ATTGATTTTG GTATAATAAA TGTGAGGCTG     900

    TTTTGCAAAC TTAAAAAAAA ATTTAAAAAA ACTGGAGGGG GGCCCGTACC CAANTCGCCG     960

40  NATATGAT                                                             968


45  (2) INFORMATION FOR SEQ ID NO: 222:

          (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1404 base pairs
              (B) TYPE: nucleic acid
50            (C) STRANDEDNESS: double
              (D) TOPOLOGY: linear

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

55  CGTTTTCCGG CCGTGCGTTT GTGGCCGTCC GGCCTCCCTG ACATGCAGCC CTCTGGACCC      60

    CGAGGTTGGA CCCTACTGTG ACACACCTAC CATGCGGACA CTCTTCAACC TCCTCTGGCT     120

    TGCCCTGGCC TGCAGCCCTG TTCACACTAC CCTGTCAAAG TCAGATGCCA AAAAAGCCGC     180
60
```

CTCAAAGACG CTGCTGGAGA AGAGTCAGTT TTCAGATAAG CCGGTGCAAG ACCGGGGTTT   240

GGTGGTGACG GACCTCAAAG CTGAGAGTGT GGTTCTTGAG CATCGCAGCT ACTGCTCGGC   300

AAAGGCCCGG GACAGACACT TTGCTGGGGA TGTACTGGGC TATGTCACTC CATGGAACAG   360

CCATGGCTAC GATGTCACCA AGGTCTTTGG GAGCAAGTTC ACACAGATCT CACCCGTCTG   420

GCTGCAGCTG AAGAGACGTG GCCGTGAGAT GTTTGAGGTC ACGGGCCTCC ACGACGTGGA   · 480

CCAAGGGTGG ATGCGAGCTG TCAGGAAGCA TGCCAAGGGC CTGCACATAG TGCCTCGGCT   540

CCTGTTTGAG GACTGGACTT ACGATGATTT CCGGAACGTC TTAGACAGTG AGGATGAGAT   600

AGAGGAGCTG AGCAAGACCG TGGTCCAGGT GGCAAAGAAC CAGCATTTCG ATGGCTTCGT   660

GGTGGAGGTC TGGAACCAGC TGCTAAGCCA GAAGCGCGTG GGCCTCATCC ACATGCTCAC   720

CCACTTGGCC GAGGCTCTGC ACCAGGCCCG GCTGCTGGCC CTCCTGGTCA TCCCGCCTGC   780

CATCACCCCC GGGACCGACC AGCTGGGCAT GTTCACGCAC AAGGAGTTTG AGCAGCTGGC   840

CCCCGTGCTG GATGGTTTCA GCCTCATGAC CTACGACTAC TCTACAGCGC ATCAGCCTGG   900

CCCTAATGCA CCCCTGTCCT GGGTTCGAGC CTGCGTCCAG GTCCTGGACC CGAAGTCCAA   960

GTGGCGAAGC AAAATCCTCC TGGGGCTCAA CTTCTATGGT ATGGACTACG CGACCTCCAA   1020

GGATGCCCGT GAGCCTGTTG TCGGGGCCAG GTACATCCAG ACACTGAAGG ACCACAGGCC   1080

CCGGATGGTG TGGGACAGCC AGGYCTCAGA GCACTTCTTC GAGTACAAGA AGAGCCGCAG   1140

TGGGAGGCAC GTCGTCTTCT ACCCAACCCT GAAGTCCCTG CAGGTGCGGC TGGAGCTGGC   1200

CCGGGAGCTG GGCGTTGGGG TCTCTATCTG GGAGCTGGCC AGGGCCTGGA CTACTTCTAC   1260

GACCTGCTCT AGGTGGGCAT TGCG̲GCCTCC GCGGTGGACG TGTTCTTTTC TAAGCCATGG   1320

AGTGAGTGAG CAGGTGTGAA ATACAGGCCT NCACTCCGTT TGCTGTGAAA AAAAAAAAAA   1380

AAAAAAAAAA AAAAAAAAAA AAAA   1404

(2) INFORMATION FOR SEQ ID NO: 223:

       (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 707 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

NGCGCGCCTG CAGTCGACAC TAGTGGATCC AAAGAATTCG GCACGAGGGC AGGTCCAGGG   60

CTCAGAAATC AGCTCTATTG ACGAATTCTG CCGCAAGTTC CGCCTGGACT GCCCGCTGGC   120

CATGGAGCGG ATCAAGGAGG ACCGGCCCAT CACCATCAAG GACGACAAGG GCAACCTCAA   180

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CCGCTGCATC GCAGACGTGG TCTCGCTCTT CATCACGGTC ATGGACAAGC TGCGCCTGGA      240

GATCCGCGCC ATGGATGAGA TCCAGCCCGA CCTGCGAGAG CTGATGGAGA CCATGCACCG      300

CATGAGCCAC CTCCCACCCG ACTTTGAGGG CCGCCAGACG GTCAGCCAGT GGCTGCAGAC      360

CCTGAGCGGC ATGTCGGCGT CAGATGAGCT GGACGACTCA CAGGTGCGTC AGATGCTGTT      420

CGACCTGGAG TCAGCCTACA ACGCCTTCAA CCGCTTCCTG CATGCCTGAG CCCGGGCAC      480

TAGCCCTTGC ACAGAAGGGC AGAGTCTGAG GCGATGGCTC CTGGTCCCCT GTCCGCCACA      540

CAGGCCGTGG TCATCCACAC AACTCACTGT CTGCAGCTGC CTGTCTGGTG TCTGTCTTTG      600

GTGTCAGAAC TTTTGGGCCG GGCCCCTCCC CACAATAAAG ATGCTCTCCG ACCTTCAAAA      660

AAAAAAAAAA AAAAACTCRG GGGGGCCCCG GTCCCAATCC CCCCNTN                    707



    (2) INFORMATION FOR SEQ ID NO: 224:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 1384 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GGGGAACTGC AGTGACAGCA GGAGTAAGAG TGGGAGGCAG GACAGAGCTG GGACACAGGT       60

ATGGAGAGGG GGTTCAGCGA GCCTAGAGAG GGCAGACTAT CAGGGTGCCG GCGGTGAGAA      120

TCCAGGGAGA GGAGCGGAAA CAGAAGAGGG GCAGAAGACC GGGGCACTTG TGGGTTGCAG      180

AGCCCCTCAG CCATGTTGGG AGCCAAGCCA CACTGGCTAC CAGGTCCCCT ACACAGTCCC      240

GGGCTGCCCT TGGTTCTGGT GCTTCTGGCC CTGGGGGCCG GGTGGGCCCA GGAGGGGTCA      300

GAGCCCGTCC TGCTGGAGGG GGAGTGCCTG GTGGTCTGTG AGCCTGGCCG AGTTGCTGCA      360

GGGGGGCCCG GGGGAGCAGC CCTGGGAGAG GCACCCCCTG GGCGAGTGGC ATTGCTGCG      420

GTCCGAAGCC AMCACCATGA GCCAGCAGGG GAAACCGGCA ATGGCACTAK TGGGGCCATC      480

TACTTCGACC AGGTCCTGGT GAACGAGGGC GGTGGCTTTG ACCGGGCTTC TGGCTCCTTC      540

GTAGCCCCTG TCCGGGGTGT CTACAGCTTC CGGTTCCATG TGGTGAAGGT GTACAACCGC      600

CAAACTGTCC AGGTGAGCCT GATGCTGAAC ACGTGGCCTG TCATCCGCGC CTTTGCCAAT      660

GATCCTGACG TGACCCGGGA GGCAGCCACC AGCTCTGTGC TACTGCCCTT GGACCCTGGG      720

GACCGAGTGT CTCTGCGCCT GCGTCGGGGG AATCTACTGG GTGGTTGGAA ACACTCAAGT      780

TTCTCTGGCT TCCTCATCTT CCCTCTCTGA GGACCCAAGT YTTTCAAGCA CAAGAATCCA      840
```

477

```
GCCCCTGACA ACTTTCTTCT GCCCTCTCTT GCCCCAGAAA CAGCAGAGGC AGGAGAGAGA        900

CTCCCTCTGG YTCCTATCCC ACYTCTTTGC ATGGGAMCCT GTGCCAAACA CCCAAGTTTA        960

AGARAARARY ARARCTGWGG CAGGTATACA GAGCTGGAAG TGGACCATGG AAAACATSGA       1020

TAACCATGCA TCYTCTTGCT TGGCCACCTC CTGAAACTGT CCACCTTTGA AGTTTGAACT       1080

TTAGTCCCTC CAMACTCTGA CTGCTGCCTC CTTCCTCCCA GCTCTCTCAC TGAGTTATYT      .1140

TCACTGTACC TGTTCCAGCA TATCCCCACT ATCTCTCTTT CTCCTGATCT GTGCTGTCTT       1200

ATTCTCCTCC TTAGGCTTCC TATTACCTGG GATTCCATGA TTCATTCCTT CAGACCCTCT       1260

CCTGCCAGTA TGCTAAACCC TCCCTCTCTC TTTCTTATCC CGCTGTCCCA TTGGCCCAGC       1320

CTGGATGAAT CTATCAATAA AACAACTAGA GAATGGTGGT CAAAAAAAAA AAAAAAAAAC       1380

TCGA                                                                    1384
```

(2) INFORMATION FOR SEQ ID NO: 225:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 760 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

```
GGGTCGACCC ACGCGTCCGC TGACCAGTCC GTTATAGATA CTTCTTCCTA TACCAAAACT         60

GTTTAAACAG GTGCCACCAC AAGGGATGTC GTCCTTACTC TCTGCGGGTC TTCAAGCATC .      120

CCTTTGTGGG AAARGTCTCT GGGCAAGCAC GTGGTATTTG GTCTGCTGCT TGCTTCCCTT        180

TTTCCACCAG GGATGTTGTG ATCATAAGTC AAAACAACAG TATATTCCAA ATCTCAAAAG        240

CTATTGTGGC CTGAGCACAA TTGAAATCTA GCAGAGTTTT TCCTATGTAG CTTTAGAGTA        300

ACTCTTCTGC TTCTCTGTCA CTTACAATTC AGGTTCTGCC TTTGCCTAAG AGCATGAGCA        360

GAAGAGTCCT CATGTGACGC TTAGTTCTAT TGCAGTCCTG GGTGAAACTA TTTAAGCWAT        420

GGGGCTGCTK CTCCCCANWT CCTCCCTAAC AATTCGTTGT GTGGACTTCT CATCTAAAAG        480

GTTAGTGGCT TTTGCTTGGG ATCAGTGCTC TCTATTGATG TTCTTGCTGG TCTCCAGACA        540

CATTCCTGTT GCATTAAGAC TTGAAAGACT TGTAGATGTG TGATGTTCAG GCACAGGATG        600

CTGAAAGCTA TGTTACTATT CTTAGTTTGT AAATTGTCCT TTTGATACCA TCATCTTGTT        660

TTCTTTTTGT AGGTATAAAT AAAAACACTG TTGACAATAA AAAAAAAAAA AAAAAAAAAA        720

AAAAAAAAAA AAAAAAAAAA NAAAAAAAAA AAAAAAAAAA                              760
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478

(2) INFORMATION FOR SEQ ID NO: 226:

5

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 2057 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

10

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

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CCGAGCCGGC TGCGCCGGGG GAATCCGTGC GGGCGCCTTC CGTCCCRGTC CCATCCTCGC      60

CGCGCTCCAG CACCTCTGAA GTTTTGCAGC GCCCAGAAAG GAGGCGAGGA AGGAGGGAGT     120

GTGTGAGAGG AGGGAGCAAA AAGCTCACCC TAAAACATTT ATTTCAAGGA GAAAAGAAAA     180

AGGGGGGGCG CAAAAATGGC TGGGGCAATT ATAGAAAACA TGAGCACCAA GAAGCTGTGC     240

ATTGTTGGTG GGATTCTGCT CGTGTTCCAA ATCATCGCCT TTCTGGTGGG AGGCTTGATT     300

GCTCCAGGGC CCACAACGGC AGTGTCCTAC ATGTCGGTGA AATGTGTGGA TGCCCGTAAG     360

AACCATCACA AGACAAAATG GTTCGTGCCT TGGGGACCCA ATCATTGTGA CAAGATCCGA     420

GACATTGAAG AGGCAATTCC AAGGGAAATT GAAGCCAATG ACATCGTGTT TTCTGTTCAC     480

ATTCCCCTCC CCACATGGA GATGAGTCCT TGGTTCCAAT TCATGMTGTT TATCCTGCAG     540

CTGGACATTG CCTTCAAGCT AAACAACCAA ATCAGRGAAA ATGCAGAAGT CTCCATGGAC     600

GTTTCCCTGG CTTACCGTGA TGACGCGTTT GCTGAGTGGA CTGAAATGGC CCATGAAAGA     660

GTACCACGGA AACTCAAATG CACCTTCACA TCTCCCAAGA CTCCAGAGCA TGGAGGGCCG     720

GTTACTATGA ATGTGATGTC CTTCCTTTCA TGGAAATTGG GTCTGTGGCC CATGAAGTTT     780

TACCTTTTAA ACATCCGGCT GCCTGTGAAT GAGAAGAAGA AAATCAATGT GGGAATTGGG     840

GAGATAAAGG ATATCCGGTT GGTGGGGATC CACCAAAATG GAGGCTTCAC CAAGGTGTGG     900

TTTGCCATGA AGACCTTCCT TACGCCCAGC ATCTTCATCA TTATGGTGTG GTATTGGAGG     960

AGGATCACCA TGATGTCCCG ACCCCCAGTG CTTCTGGAAA AAGTCATCTT TGCCCTTGGG    1020

ATTTCCATGA CCTTTATCAA TATCCCAGTG GAATGGTTTT CCATCGGGTT TGACTGGACC    1080

TGGATGCTGC TGTTTGGTGA CATCCGACAG GCATCTTCTA TGCRATGCTT CTKTCCTTCT    1140

GGATCATCTT CTGTGGCGAG CACATGATGG ATCAGCACGA GCGGAACCAC ATCGCAGGGT    1200

ATTGGAAGCA AGTCGGACCC ATTGCCGTTG GTCCTTCTGC CTCTTCATAT TTGACATGTG    1260

TGAGAGAGGG GTACAACTCA CGAATCCCTT CTACAGTATC TGGACTACAG ACATTGGGAA    1320

CAGAGCTGGC CATGGCTTTC ATCATCGTGG CTGGAATCTG CCTCTGCCTC TAACTTCCTG    1380

TTTCTATGCT TCATGGTATT TCAGGTGTTT CGGAACATCA GTGGAAGCA GTCCAGCCTG    1440
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60

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CCAGCTATGA GCAAGTCCG GCGGCTACAC TATGAGGGGC TAATTTTTAG GTTCAAGTTC       1500

CTCATGCTTA TCACCTTGGC TTGCGCTGCC ATGACTGTCA TCTTCTTCAT CGTTAGTCAG       1560

GTAACGGAAG GCTATTGGA AATGGGGCGG CGTCACAGTC CCAAGTGAAC AGTGCCTTTT       1620

TCACAGGCAT CTATGGGATG TGGAATCTGT ATGTCTTTGC TCTGATGTTC TTGTATGCAC       1680

CATCCCATAA AAACTATGGA GAAGACCAGT CCATGGAAT GCAACTCCCA TGTAAATCGA       1740

GGGAAGATTG TGCTTTGTTT GTTTCGGAAC TTTATCAAGA ATTGTTCAGC GCTTCGAAAT       1800

ATTCCTTCAT CAATGACAAC GTAGCTTCTG GTATTTGAGT CAACAAGGCA ACACATGTTT       1860

ATCAGCTTTG CATTTGCAGT TTTCACAGTC ACATTGATTG TACTTGTATA CGCACACAAA       1920

TACACTCATT TAGCCTTTAT CTCAAAATGT TAAATATAAG GAAAAAAGCG TCAACAATAA       1980

ATATTCTTTG AGTATTGTCT TACTTCTCTT AAAAAAAAAA AAAAAAACTC GTGCCGAATT       2040

CGGCACGAGC GGCACGA                                                     2057
```

(2) INFORMATION FOR SEQ ID NO: 227:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 2084 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: double
            (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

```
GGCAGAGGGC CATTTCCTGC AAAGAGCCAA ACCCCCATTC CTCTGTGCCC CTCCTCTCCC        60

ACCAAGTGCT TTATAAAAT AGCTCTTGTT ACCGGAAATA ACTGTTCATT TTTCACTCCT       120

CCCTCCTAGG TCACACTTTT CAGAAAAAGA ATCTGCATCC TGGAAACCAG AAGAAAAATA       180

TGAGACGGGG AATCATCGTG TGATGTGTGT GCTGCCTTTG GCTGAGTGTG TGGAGTCCTG       240

CTCAGGTGTT AGGTACAGTG TGTTTGATCG TGGTGGCTTG AGGGGAACCG CTTGTTCAGA       300

GCTGTGACTG CGGCTGCACT GTAGAGAAGC TGCCCTTGGC TGCTCGTAGC GCCGGGCCTT       360

CTCTCCTCGT CATCATCCAG AGCAGCCAGT GTCCGGGAGG CAGAAGGTAC CGGGGCAGCT       420

ACTGGAGGAC TGTGCGGCC TGCCTGGGCT GCCCCCTCCG CCGTGGGGCC CTGTTGCTGC       480

TGTCCATCTA TTTCTACTAC TCCCTCCCAA ATGCGGTCGG CCCGCCCTTC ACTTGGATGC       540

TTGCCCTCCT GGGCCTTCTC GCAGGCACTG AACATCCTCC TGGGCCTCAA GGGCCTGGCC       600

CCAGCTGAGA TCTCTGCAGT GTGTGAAAA GGGAATTTCA ACGTGGCCCA TGGGCTGGCA       660

TGGTCATATT ACATCGGATA TCTGCGGCTG ATCCTGCCAG AGCTCCAGGC CCGGATTCGA       720

ACTTACAATC AGCATTACAA CAACCTGCTA CGGGGTGCAG TGAGCCAGCG GTGTNATATT       780
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CTCCTCCCAT TGGACTGTGG GGTGCCTGAT AACCTGAGTA TGGCTGACCC CAACATTCGC    840

TTCCTGGATA AACTGCCCCA GCAGACCGGT GACCGTGCTG GCATCAAGGA TCGGGTTTAC    900

AGCAACAGCA TCTATGAGCT TCTGGAGAAC GGGCAGCGGG CGGGCACCTG TGTCCTGGAG    960

TACGCCACCC CCTTGCAGAC TTTGTTTGCC ATGTCACAAT ACAGTCAAGC TGGCTTTAGC   1020

GGGGAGGATA GGCTTGAGCA GGCCAAACTC TTCTGCCGGA CACTTGAGGA CATCCTGGCA   1080

GATGCCCCTG AGTCTCAGAA CAACTGCCGC CTCATTGCCT ACCAGGAACC TGCAGATGAC   1140

AGCAGCTTCT CGCTGTCCCA GGAGGTTCTC CGGCACCTGC GGCAGGAGGA AAAGGAAGAG   1200

GTTACTGTGG GCAGCTTGAA GACCTCAGCG GTGCCCAGTA CCTCCACGAT GTCCCAAGAG   1260

CCTGAGCTCC TCATCAGTGG AATGGAAAAG CCCCTCCCTC TCCGCACGGA TTTCTCTTGA   1320

GACCCAGGGT CACCAGGCCA GAGCCTCCAG TGGTCTCCAA GCCTCTGGAC TGGGGGCTCT   1380

CTTCAGTGGC TGAATGTCCA GCAGAGCTAT TTCCTTCCAC AGGGGGCCTT GCAGGGAAGG   1440

GTCCAGGACT TGACATCTTA AGATGCGTCT TGTCCCCTTG GGCCAGTCAT TTCCCCTCTC   1500

TGAGCCTCGG TGTCTTCAAC CTGTGAAATG GGATCATAAT CACTGCCTTA CCTCCCTCAC   1560

GGTTGTTGTG AGGACTGAGT GTGTGGAAGT TTTTCATAAA CTTTGGATGC TAGTGTACTT   1620

AGGGGGTGTG CCAGGTGTCT TTCATGGGGC CTTCCAGACC CACTCCCCAC CCTTCTCCCC   1680

TTCCTTTGCC CGGGGACGCC GAACTCTCTC AATGGTATCA ACAGGCTCCT TCGCCCTCTG   1740

GCTCCTGGTC ATGTTCCATT ATTGGGGAGC CCCAGCAGAA GAATGGAGAG GAGGAGGAGG   1800

CTGAGTTTGG GGTATTGAAT CCCCCGGCTC CCACCCTGCA GCATCAAGGT TGCTATGGAC   1860

TCTCCTGCCG GGCAACTCTT GCGTAATCAT GACTATCTCT AGGATTCTGG CACCACTTCC   1920

TTCCCTGGCC CCTTAAGCCT AGCTGTGTAT CGGCACCCCC ACCCCACTAG AGTACTCCCT   1980

CTCACTTGCG GTTTCCTTAT ACTCCACCCC TTTCTCAACG GTCCTTTTTT AAAGCACATC   2040

TCAGATTAAA AAAAAAAAA AAAAAAAAA AGGGGGGGCN GCNT   2084
```

(2) INFORMATION FOR SEQ ID NO: 228:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2143 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

```
TCGACCCACG CGTCCGGTTG AATTCCTTGA CCTGCAAACA CATATTTATT AGCCTGACTC    60
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AAACAATGAA GCTATTAAAA CTTCGGAGGA ACATTGTAAA ACTCTCTTTG TATCGGCATT        120

TCACCAACAC GCTTATTTTG GCAGTGGCAG CATCCATTGT GTTTATCATC TGGACAACCA        180

TGAAGTTCAG AATAGTGACA TGTCAGTCGG ACTGGCGGGA GCTGTGGGTA GACGATGCCA        240

TCTGGCGCTT GCTGTTCTCC ATGATCCTCT TTGTCATCAT GGTTCTCTGG CGACCATCTG        300

CAAACAACCA GAGGTTTGCC TTTTCACCAT TGTCTGAGGA AGAGGAGGAG GATGAACAAA        360

AGGAGCCTAT GCTGAAAGAA AGCTTTGAAG GAATGAAAAT GAGAAGTACC AAACAAGAAC        420

CCAATGGAAA TAGTAAAGTT AACAAAGCAC AGGAAGATGA TTTGAAGTGG GTAGAAGAGA        480

ATGTTCCTTC TTCTGTGACA GATGTAGCAC TTCCAGCCCT TCTGGATTCA GATGAGGAAC        540

GAATGATCAC ACACTTTGAA AGGTCCAAAA TGGAGTAAGG AATGGGAAGA TTTGCAGTTA        600

AAGATGGCTA CCATCAGGGA AGAGATCAGC ATCTGTGTCA GTCTTCTGTA CGGCTCCATG        660

GGATTAAAGG AAGCAATGAC ATCCTGATCT GTTCCTTGAT CTTTGGGCAT TGGAGTTGGC        720

GAGAGGTGTC AGAACAAAGA GAACATCTTA CTGAAAACAA GTTCATAAGA TGAGAAAAAT        780

CTACGAGCTT CTTATTTACA ACACTGCTGC CCCCTTTCCT CCCAGACTCT GACATGGATG        840

TTCATGCAAC TTAAGTGTGT TGTTCCTGAA CTTTCTGTAA TGTTTCATTT TTTAAATCTG        900

ACAAACTAAA AAGTTTAACG TCTTCTAAAA GATTGTCATC AACACCATAA TATGTAATCT        960

CCAGGAGCAA CTGCCTGTAA TTTTTATTTA TTTAGGGAGT TACATAGGTG ATGGGGGAAA       1020

TTGTTAACTA CCTTTCATTT TCCTGGGAAG TCAAGGTTAC ATCTTGCAGA GGTTGTTTTG       1080

AGAAAAAAGG GCCCTTCTGA GTTAAGGAGC CATAGTTCTA TCAATGATCA AAAGAAAAAA       1140

AAAAAAAAGA GAAACTGTTA CAGTATGATT CAGATCATTT AAAAAAGCAA AATCAAGTGC       1200

AATTTTGTTT ACAAATGGTG TATATTAAAG ATTTTTCTAT TTCAGATGTA CTTTAAAGAG       1260

AAATATTAGC TTAACTCTTT TGACATCTGC TATTGTGACA CATCCCATTG CTGGCAATGT       1320

GGTGCACACT CCGAAACTTT TAACTACTGT TTTGTAAGCC TCCAAGGGTG GCATTGCAGG       1380

GTCCTTAGGC AATGTTTTGT TTGCCTTTAT GCAGAGAGGT GCTCCAAGTG CTGTGATTGA       1440

GCACCGTGCT AGAGGAACTG TAATGCTTCA GAAGTTGTAG CTTATACAAA GGAAACAGGT       1500

CCTGCTGGCT TAATTTAAAC AGTTATTGCA TGAAGTAGCG TGGAGGCCCT GGACTGCTGC       1560

TCGTTCTTTA GGATGGACTG TTCTGGTATC TGGTATTGGT TTAGAGACTG TTAATAAGGG       1620

ACATCACAAG GTGATGGGAT TCATTTGAAG CACTCTATTT CTGTTTTAAT GGTTTTATCC       1680

AATTTTGCCT TCCCAAGATT TTTGTTCTAC ATAAAAAGTT CATGCCACTT TTTAATATAA       1740

AAAAATTTAA CAAAATTAAT GTATTTTTCT CATTTTTTTC AAACTTTTTC TAAAGACTCT       1800

TTCTGTCAAA CTCATGAAAA ATTTCTTTCT ATGGCTTTTA TTCTAGATTG TCTTATTTTC       1860
```

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TGTTAAAACC AATGACCACA TGACCACAAT CTTCACTAAC TCATACTGCA GTGAAAGTGT   1920

TAACCCTTAG GTAGTTTCTC TACAACTCTT TGCTATGGTG ATTTTTAAAA AAGTTTCCTA   1980

GGGAAGTATC TCTGAGGGAA CAGGCAATCT GAAGGAACTG ACTATATTCT CCATGGCTAA   2040

GTCCATTAGG CCAAAAGNCT GGGTGGGTAT TGGTTGTCAN GCTGTCTATT GGCATATTAA   2100

AAACGTAGGC CGGANGGAAT AATTAGGTTG TNATGCCGGC GGG   2143

(2) INFORMATION FOR SEQ ID NO: 229:

        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1025 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: double
                (D) TOPOLOGY: linear

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

CCTGGCCCAC ATTGCTTCAT TGGCCTGGCC ATGCGCCTGT ACTATGGCAG CCGCTAGTCC   60

CTGACAACTT CCACCCTGAT TCCGGACCCT GTAGATTGGG CGCCACCACC AGATCCCCCT   120

CCCAGGCCTT CCTCCCTCTC CCATCAGCAG CCCTGTAACA AGTGCCTTGT GAGAAAAGCT   180

GGAGAAGTGA GGGCAGCCAG GTTATTCTCT GGAGGTTGGT GGATGAAGGG GTACCCTAGG   240

AGATGTGAAG TGTGGGTTTG GTTAAGGAAA TGCTTACCAT CCCCCACCCC CAACCAAGTT   300

CTTCCAGACT AAAGAATTAA GGTAACATCA ATACCTAGGC CTGAGAAATA ACCCCATCCT   360

TGTTGGGCAG CTCCCTGCTT TGTCCTGCAT GAACAGAGTT GATGAAAGTG GGGTGTGGGC   420

AACAAGTGGC TTTCCTTGCC TACTTTAGTC ACCCAGCAGA GCCACTGGAG CTGGCTAGTC   480

CAGCCCAGCC ATGGTGCATG ACTCTTCCAT AAGGGATCCT CACCCTTCCA CTTTCATGCA   540

AGAAGGCCCA GTTGCCACAG ATTATACAAC CATTACCCAA ACCACTCTGA CAGTCTCCTC   600

CAGTTCCAGC AATGCCTAGA GACATGCTCC CTGCCCTCTC CACAGTGCTG CTCCCCACAC   660

CTAGCCTTTG TTCTGGAAAC CCCAGAGAGG GCTGGGCTTG ACTCATCTCA GGGAATGTAG   720

CCCCTGGGCC CTGGCTTAAG CCGACACTCC TGACCTCTCT GTTCACCCTG AGGGCTGTCT   780

TGAAGCCCGC TACCCACTCT GAGGCTCCTA GGAGGTACCA TGCTTCCCAC TCTGGGGCCT   840

GCCCCTGCCT AGCAGTCTCC CAGCTCCCAA CAGCCTGGGG AAGCTCTGCA CAGAGTGACC   900

TGAGACCAGG TACAGGAAAC CTGTAGCTCA ATCAGTGTCT CTTTAACTGC ATAAGCAATA   960

AGATCTTAAT AAAGTCTTCT AGGCTGTAGG GTGGTTCCTA CAACCACAGC CAAAAAAAAA   1020

AAAAA   1025

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(2) INFORMATION FOR SEQ ID NO: 230:

5   (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 1250 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: double
               (D) TOPOLOGY: linear
10
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

GCCCACGCGT CCGCCCACGC GTCCGGCGGT GCGGAGTATG GGGCGCTGAT GGCCATGGAG   60

15   GGCTACTGGC GCTTCCTGGC GCYGCTGGGG TCGGCACTGC TCGTCGGCTT CCTGTCGGTG   120

ATSTTCGCCC TCGTCTGGGT CCTCCACTAC CGAGAGGGGC TTGGCTGGGA TGGGAGCGCA   180

CTAGAGTTTA ACTGGCACCC AGTGCTSATG GTCACCGGCT TCGTCTTCAT CCAGGGCATC   240
20
GCATCATCGT CTACAGACTG CCGTGGACCT GGAAATGCAG CAAGCTCCTG ATGAAATCCA   300

TCCATGCAGG GTTAAATGCA GTTGCTGCCA TTCTTGCAAT TATCTCTGTG GTGGCCGTGT   360

TTGAGAACCA CAATGTTAAC AATATAGCCA ATATGTACAG TCTGCACAGC TGGGTTGGAC   420
25
TGATAGCTGT CATATGCTAT TTGTTACAGC TTCTTTCAGG TTTTTCAGTC TTTCTGCTTC   480

CATGGGCTCC GCTTTCTCTC CGAGCATTTC TCATGCCCAT ACATGTTTAT TCTGGAATTG   540
30
TCATCTTTGG AACAGTGATT GCAACAGCAC TTATGGGATT GACAGAGAAA CTGATTTTTT   600

CCCTGAGAGA TCCTGCATAC AGTACATTCC CGCCAGAAGG TGTTTTCGTA AATACGCTTG   660

35   GCCTTCTGAT CCTGGTGTTC GGGGCCCTCA TTTTTTGGAT AGTCACCAGA CCGCAATGGA   720

AACGTCCTAA GGAGCCAAAT TCTACCATTC TTCATCCAAA TGGAGGCACT GAACAGGGAG   780

CAAGAGGTTC CATGCCAGCC TACTCTGGCA ACAACATGGA CAAATCAGAT TCAGAGTTAA   840
40
ACARTGAAGT AGCAGCAAGG AAAAGAAACT TAGCTCTGGA TGAGGCTGGG CAGAGATCTA   900

CCATGTAAAA TGTTGTAGAG ATAGAGCCAT ATAACGTCAC GTTTCAAAAC TAGCTCTACA   960

45   GTTTTGCTTC TCCTATTAGC CATATGATAA TTGGGCTATG TAGTATCAAT ATTTACTTTA   1020

ATCACAAAGG ATGGTTTCTT GAAATAATTT GTATTGATTG AGGCCTATGA ACTGACCTGA   1080

ATTGGAAAGG ATGTGATTAA TATAAATAAT AGCAGATATA AATTGTGGTT ATGTTACCTT   1140
50
TATCTTGTTG AGGACCACAA CATTAGCACG GTGCCTTGTG CAKAATAGAT ACTCAATATG   1200

TGAATATGTG TCTACTAGTA GTTAATTGGA TAAACTGGCA GCATCCCTGA   1250

55

(2) INFORMATION FOR SEQ ID NO: 231:

60   (i) SEQUENCE CHARACTERISTICS:

           (A) LENGTH: 1811 base pairs
           (B) TYPE: nucleic acid
           (C) STRANDEDNESS: double
           (D) TOPOLOGY: linear

5

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CNGNCAGTAC CGGTCNGATT CCCGGGTCGA CCCACGCGTC CGCTGCATTC CAGGGCCTTT   .   60

10   CAGTGGCTTT CATTCTGAAG TTCCTGGATA ACATGTTCCA TGTCTTGATG GCCCAGGTTA   120

CCASTGTCAT TATCACAACA GTGTCTGTCC TGGTCTTTGA CTTCAGGCCC TCCCTGGAAT   180

TTTTCTTGGA AGCCSCATCA GTCSTYCTCT CTATATTTAT TTATAATGCC AGCAAGCCTC   240

15

AAGTTCCGGA ATACGCACCT AGGCAAGAAA GGATCCGAGA TCTAAGTGGC AATCTTTGGG   300

AGCGTTCCAG TGGGGATGGA GAAGAACTAG AAAGACTTAC CAAACCCAAG AGTGATGAGT   360

20   CAGATGAAGA TACTTTCTAA CTGGTACCCA CATAGTTTGC AGCTCTCTTG AACCTTATTT   420

TCACATTTTC AGTGTTTGTA ATATTTATCT TTTCACTTTG ATAAACCAGA AATGTTTCTA   480

AATCCTAATA TTCTTTGCAT ATATCTAGCT ACTCCCTAAA TGGTTCCATC CAAGGCTTAG   540

25

AGTACCCAAA GGCTAAGAAA TTCTAAAGAA CTGATACAGG AGTAACAATA TGAAGAATTC   600

ATTAATATCT CAGTACTTGA TAAATCAGAA AGTTATATGT GCAGATTATT TTCCTTGGCC   660

30   TTCAAGCTTC CAAAAAACTT GTAATAATCA TGTTAGCTAT AGCTTGTATA TACACATAGA   720

GATCAATTTG CCAAATATTC ACAATCATGT AGTTCTAGTT TACATGCCAA AGTCTTCCCT   780

TTTTAACATT ATAAAAGCTA GGTTGTCTCT TGAATTTTGA GGCCCTAGAG ATAGTCATTT   840

35

TGCAAGTAAA GAGCAACGGG ACCCTTTCTA AAAACGTTGG TTGAAGGACC TAAATACCTG   900

GCCATACCAT AGATTTGGGA TGATGTAGTC TGTGCTAAAT ATTTTGCTGA AGAAGCAGTT   960

40   TCTCAGACAC AACATCTCAG AATTTTAATT TTTAGAAATT CATGGGAAAT TGGATTTTTG   1020

TAATAATCTT TTGATGTTTT AAACATTGGT TCCCTAGTCA CCATAGTTAC CACTTGTATT   1080

TTAAGTCATT TAAACAAGCC ACGGTGGGGC TTTTTTCTCC TCAGTTTGAG GAGAAAAATC   1140

45

TTGATGTCAT TACTCCTGAA TTATTACATT TTGGAGAATA AGAGGGCATT TTATTTTATT   1200

AGTTACTAAT TCAAGCTGTG ACTATTGTAT ATCTTTCCAA GAGTTGAAAT GCTGGCTTCA   1260

50   GAATCATACC AGATTGTCAG TGAAGCTGAT GCCTAGGAAC TTTTAAAGGG ATCCTTTCAA   1320

AAGGATCACT TAGCAAACAC ATGTTGACTT TTAACTGATG TATGAATATT AATACTCTAA   1380

AAATAGAAAG ACCAGTAATA TATAAGTCAC TTTACAGTGC TACTTCACAC TTAAAAGTGC   1440

55

ATGGTATTTT TCATGGTATT TTGCATGCAG CCAGTTAACT CTCGTAGATA GAGAAGTCAG   1500

GTGATAGATG ATATTAAAAA TTAGCAAACA AAAGTGACTT GCTCAGGGTC ATGCAGCTGG   1560

60   GTGATGATAG AAGAGTGGGC TTTAACTGGC AGGCCTGTAT GTTTACAGAC TACCATACTG   1620

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TAAATATGAG CTTTATGGTG TCATTCTCAG AAACTTATAC ATTTCTGCTC TCCTTTCTCC    1680

TAAGTTTCAT GCAGATGAAT ATAAGGTAAT ATACTATTAT ATAATTCATT TGTGATATCC    1740

ACAATAATAT GACTGGCAAG AATTGGTGGA AATTTGTAAT TAAAATAATT ATTAAACCTA    1800

AAAAAAAAAN N                                                          1811
```

(2) INFORMATION FOR SEQ ID NO: 232:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2271 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

```
CTGACCTCAT GGCGTAGAGC CTAGCAACAG CGCAGGCTCC CAGCCGAGTC CGTTATGGCC     60

GCTGCCGTCC CGAAGAGGAT GAGGGGGCCA GCACAAGCGA AACTGCTGCC CGGGTCGGCC    120

ATCCAAGCCC TTGTGGGGTT GGCGCGGCCG CTGGTCTTGG CGCTCCTGCT TGTGTCCGCC    180

GCTCTATCCA GTGTTGTATC ACGGACTGAT TCACCGAGCC CAACCGTACT CAACTCACAT    240

ATTTCTACCC CAAATGTGAA TGCTTTAACA CATGAAAACC AAACCAAACC TTCTATTTCC    300

CAAATCAGCA CCACCCTCCC TCCCACGACG AGTACCAAGA AAAGTGGAGG AGCATCTGTG    360

GTCCCTCATC CCTCGCCTAC TCCTCTGTCT CAAGAGGAAG CTGATAACAA TGAAGATCCT    420

AGTATAGAGG AGGAGGATCT TCTGATGCTG AACAGTTCTC CATCCACAGC CAAAGACACT    480

CTAGACAATG GCGATTATGG AGAACCAGAC TATGACTGGA CCACGGGCCC CAGGGACGAC    540

GACGAGTCTG ATNGACACCT TGGAAGAAAA CAGGGGTTAC ATGGAAATTG AACAGTCAGT    600

GAAATCTTTT AAGATGCCAT CCTCAAATAT AGAAGAGGAA GACAGCCATT TCTTTTTTCA    660

TCTTATTATT TTTGCTTTTT GCATTGCTGT TGTTTACATT ACATATCACA ACAAAAGGAA    720

GATTTTTCTT CTGGTTCAAA GCAGGAAATG GCGTGATGGC CTTTGTTCCA AAACAGTGGA    780

ATACCATCGC CTAGATCAGA ATGTTAATGA GGCAATGCCT TCTTTGAAGA TTACCAATGA    840

TTATATTTTT TAAAGCACTG TGATTTGAAT TTGCTTATGT AATTTTATTT GCTTGACTTT    900

TTATATGATA TTGTGCAAAT GTTTGCCATA GGCAATTGGT ACTTAAATGA GAGGTGAGTC    960

TCTCTTTTGC CTTGGTGCTT TGGAAATTAA ATGTCACAAA CGAGTATATA ATTTTTTATC   1020

TGTACTTTTA GAGCTGAGTT TAATCAGGTG TCCAAAATGT GAGTTAAACA TTACCTTATA   1080

TTTACACTGT TAGTTTTTAT TGTTTTAGAT TTATTATGCT TCTTCTGGAA GTATTAGTGA   1140
```

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TGCTACTTTT AAAAGATCCC AAACTTGTAA CTAAATTCTG ACATATCTGT TACTGCTGAC        1200

TCACATTCAT TCTCCGCCAT TCAAATACTA TTTTTTATCC ACATTTTTTT TTGTTCCCAA        1260

ACTGTAATGT ACAAGGATAT GTGTGATAAT GCTTTGGATT TGAGTAATAT TTTTTTTTCT        1320

TCCAAGAAAA CTGCTTTGGA TATTTTTAGA TAATTTAAAC ATAATTTAGG ATAATGATAT        1380

TGCTCAATCT GACCACAATT TTAGGTAAAA CATTAAATGT GTCAAGAAAT CTTGGCAACA        1440

GAGACTCTGC AGCTTGCAGT GGACATAGAT AAAATGTTAC AGAGATACTA TTTTTTTGGT        1500

TGGAATTACT ATATTAAATT TAGAAGCAGA AACTGGTAAA ATGTTAAATA CATGTACAAT        1560

TGCTTTTAGT TAGCAATTGA TTGTAGCATG GGTTCCTCCA AGGTTTCAAG CAATGGGCAG        1620

AGTTTAAAAT TATATCAGAT TCGTTTACTT CGTTTATTAT TTTACAGTAA ATTTGAATAA        1680

ATCTTAGGGG TCATTATCAC TTAAATAATA CTGTACCTAG GTCTTTCAAA TTAAAATTAT        1740

ACCTGAATGA AGTTGTTTGT ATACATAAAG GATATTTGTG TACAATTACC TTTTTTCCCC        1800

CACACTTGTT TTCTTTGTTT TTGTTTTTTA TGGCAACTGG AAAGTATTTA CTATGGGATT        1860

CATTTATGTC TGTCTTTCTA TCATAAAGAA TTGATCAATA TGTAAATATG TGATTTGAAC        1920

CATGGTTGAC TTACAAGTGT CACTACAGCT TTTTAGAAAA CATAGCCCTA ATATATGTTA        1980

AGCAGGACCC GGGTGAGCCA GTGGGCTTGC GCTTTATGTA GAGCTGGAAG AAGGCCGTCC        2040

ATCCTGTCTC TTGGGCGGAC AGTGTACTTT CCTAATAGGG AAGGGAAGCA CAATGGAAAT        2100

ACCCCTGAAC CGTTTTATTG CAGTAATTTT TTTCATATCT GAAACTATTA TTTAATATTT        2160

TGAATAAGAT TTTAAAAAAT AAATGGCAAA GATATAAATC TAAAAAAAAA AAAAAAAAA        2220

AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAANANA N               2271
```

(2) INFORMATION FOR SEQ ID NO: 233:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1338 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

```
CTTCCGGTTC TCCGGGCAGC TGCCACTGCT GTAGCTTCTG CCACCTGCCA CGACCGGGCC         60

TCTCCCTGGC GTTTGGTCAC CTCTGCTTCA TTCTCCACCG CGCCTATGGT CCCTCTTGGA        120

GCCAGCGTGG CGNGCCTGGC GGCTCCCGGG TGGTGAGAGA GCGGTCCGGG AACGATGAAG        180

GCCTCGCAGT GCTGCTGCTG TCTCAGCCAC CTCTTGGCTT CCGTCCTCCT CCTGCTGTTG        240

CTGCCTGAAC TAAGCGGGYC CCTGGMAGTC CTGCTGCAGG CAGCCGAGGC CGCGCCAGGT        300
```

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YTTGGGCCTC CTGACCCTAG ACCAGGACAT TACCGCCGCT GCCACCGGGC CCTWACCCCT   360

GCCCAGCAGC CGGGCCGTGG TCTGGCTGAA GCTGCGGGGG CCGCGGGGCT CCGAGGGAGG   420

CAATGGCAGC AACCCTGTGG CCGGGCTTGA GACGGACGAT CACGGAGGGA AGGCCGGGGA   480

ARGCTCGGTG GGTGGCGGCC TTGCTGTGAG CCCCAACCCT GGCGACAAGC CCATGACCCA   540

GCGGGCCCTG ACCGTGTTGA TGGTGGTGAG CGGCGCGGTG CTGGTGTACT TCGTGGTCAG   600

GACGGTCAGG ATGAGAAGAA GAAACCGAAA GACTAGGAGA TATGGAGTTT TGGACACTAA   660

CATAGAAAAT ATGGAATTGA CACCTTTAGA ACAGGATGAT GAGGATGATG ACAACACGTT   720

GTTTGATGCC AATCATCCTC GAAGATAAGA ATGTGCCTTT TGATGAAAGA ACTTTATCTT   780

TCTACAATGA AGAGTGGAAT TTCTATGTTT AAGGAATAAG AAGCCACTAT ATCAATGTTG   840

GGGGGGTATT TAAGTTACAT ATATTTNAAC AACCTTTAAT TTGCTGTTGC AATAAATACC   900

GTATCCTTTT ATTATATCTT TATATGTATA GAAGTACTCT GTTAATGGGC TCAGAGATGT   960

TGGGGATAAA GTATACTGTA ATAATTTATC TGTTTGAAAA TTACTATAAA ACGGTGTTTT   1020

CTGRTCGGTT TTTGTTTCCT GCTTACCATA TGATTGTAAA TTGTTTTATG TATTAATCAG   1080

TTAATGCTAA TTATTTTTGC TGATGTCATA TGTTAAAGAG CTATAAATTC CAACAACCAA   1140

CTGGTGTGTA AAAATAATTT AAAATYTCCT TTACTGAAAG GTATTTCCCA TTTTTGTGGG   1200

GAAAAGAAGC CAAATTTATT ACTTTGTGTT GGGGTTTTTA AAATATTAAG AAATGTCTAA   1260

GTTATTGTTT GCAAAACAAT AAATATGATT TTAAATTCTC TTAAAAAAAA AAAAAAAAC   1320

CCCGGGGGGG GGCCCGGN   1338

(2) INFORMATION FOR SEQ ID NO: 234:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 31 amino acids
              (B) TYPE: amino acid
              (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

Met Leu Ser Thr Gly Ile Glu Val Ala Arg Pro Pro Ala Thr Leu Leu
 1   5   10   15

Gly Leu Met Phe Val Leu Thr Gly Met Pro Arg Gly Leu Arg Xaa
            20   25   30

(2) INFORMATION FOR SEQ ID NO: 235:

        (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 116 amino acids

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```
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

  Met Asn Val Val Ile Val Ile Ile Leu Phe Ser Phe Asp Ser Val Gly
   1           5                   10              15

  Thr Met Phe Ser Cys Asn Arg Ile Pro Lys Ile Thr Val Leu Asn Lys
             20              25          30

  Leu Lys Phe Xaa Cys Glu Val Leu Leu Arg Ile Gln Thr Ile Gln Gly
         35              40              45

  Phe Tyr Arg Cys Thr Arg Ile Ser Arg Tyr Lys Gly Ile Phe Pro Asp
     50              55          60

  Phe Cys Gln Ser Gln Cys Met Gly Cys Asn Pro Glu Ser Xaa Met Ala
   65              70              75              80

  Val Pro Ala Leu Val Thr Pro Ile Leu Ala His Arg Lys Lys Glu Lys
                 85              90              95

  Gly Met Cys Leu Phe Thr Leu Ile Ile Ala Pro Thr Arg Cys Thr His
             100             105             110

  Tyr Phe Cys Xaa
         115
```

(2) INFORMATION FOR SEQ ID NO: 236:

```
             (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 103 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

  Met Ser Ser Ala Lys Ile Val Arg Gln Arg Gly Ala Val Pro Thr Tyr
   1           5                   10              15

  Tyr Thr Thr Glu Ala Gly Glu Ile Ile Phe Leu Val Leu Asn Trp Ser
             20              25              30

  Leu Ser Ile Leu His Ile Val Asp Val Leu Cys Ser Lys Pro Glu Lys
         35              40              45

  Ser Val Thr Glu Asp Ala Ala Ser Gly Leu Ser Gln Arg Met Thr Ala
     50              55              60

  Leu Val Trp Arg Lys Gly Pro Asp Gly Gly Ser Arg Lys Pro Ile Leu
   65              70              75              80

  Leu Leu Phe Phe Phe Leu Pro Leu Ile Leu Cys Phe His Ser Phe Ile
             85              90              95

  His Ser Ser Asn Ile Cys Xaa
             100
```

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(2) INFORMATION FOR SEQ ID NO: 237:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 42 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

```
Met Ile Leu Phe Pro Gln Xaa Ala Leu Arg Leu Gly Xaa Trp Pro Arg
 1               5                  10                  15

Thr Trp Ser Ile Leu Xaa Lys Tyr Ser Val Asn Phe Phe Ser Ala Tyr
                20                  25                  30

Ser Pro Met Gly Ala Val Gly Thr Glu Phe
            35                  40
```

(2) INFORMATION FOR SEQ ID NO: 238:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 37 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

```
Met Ile Ile Leu Leu Leu Phe Met Leu Leu Asn Asn Val Val Leu Val
 1               5                  10                  15

Gln Glu Asp Asn Cys Gln Arg Lys Asn Thr Val Gln Glu Arg Arg Xaa
                20                  25                  30

Trp Ser Gln Trp Xaa
            35
```

(2) INFORMATION FOR SEQ ID NO: 239:

      (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 128 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

```
Met Ala Ala Xaa Pro Pro Gly Cys Thr Pro Pro Xaa Leu Leu Asp Ile
 1               5                  10                  15

Ser Trp Leu Thr Glu Ser Leu Gly Ala Gly Gln Pro Val Pro Val Glu
                20                  25                  30

Cys Arg His Arg Leu Glu Val Ala Gly Pro Arg Lys Gly Pro Leu Ser
            35                  40                  45

Pro Ala Trp Met Pro Ala Tyr Ala Cys Gln Arg Pro Thr Pro Leu Thr
            50                  55                  60

His His Asn Thr Gly Leu Ser Glu Leu Leu Glu His Gly Val Cys Glu
```

490

```
         65                    70                 75                 80
     Glu Val Glu Arg Val Arg Arg Ser Glu Arg Tyr Gln Thr Met Lys Val
                     85                 90                 95
5
     Arg Arg Ala Gly Leu Gly Pro Thr Pro Gly Met Ser Cys Pro Gly Asn
                 100                105                110
     Asp Asn Thr Val His Thr Met His Gly Glu Ala Asn Arg Gly Ser Xaa
10               115                120                125
```

15

(2) INFORMATION FOR SEQ ID NO: 240:

    (i) SEQUENCE CHARACTERISTICS:
20
        (A) LENGTH: 67 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

```
25   Met Ser Ile Leu Cys Cys Pro Xaa Leu Cys Leu Phe Phe Ser Phe Cys
      1               5                10                 15
     Ile Ser Ser Gly Ser Cys Pro Phe Ser His Val Ser Gln Leu Ser Phe
                 20                 25                 30
30
     Ile Ala Thr Phe Ser Gln Ser Ser Pro Val Leu Leu Val Pro Ala Tyr
             35                 40                 45
     Asn Thr Tyr Leu Ser Phe Leu Ala Phe Leu Asp Cys Ala Ser Leu Thr
35           50                 55                 60
     Ser Thr Xaa
      65
```

40

(2) INFORMATION FOR SEQ ID NO: 241:

    (i) SEQUENCE CHARACTERISTICS:
45
        (A) LENGTH: 69 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

```
50   Met Ser Thr Phe Gln Leu Leu Leu Ile Leu Ala Gln Ser Thr Tyr
      1               5                10                 15
     Lys Ile Lys Ser Lys Pro Leu His Met Thr Asn His Thr Leu Leu Asn
                 20                 25                 30
55
     Ser Pro Gly Leu Asn Pro Ser Ser Pro Thr Leu Asn Phe Lys Thr Gln
             35                 40                 45
     Gln His Glu Ser Val Ser Tyr Ala Cys Cys His Met Arg Ser Leu His
60           50                 55                 60
```

491

His Ala Phe Ala Xaa
 65

(2) INFORMATION FOR SEQ ID NO: 242:

          (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 44 amino acids
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

Met Val Ser Val Val Leu Ile Phe Ser Phe Leu Ser Leu Thr Ile Ser
 1   5   10   15

Thr Thr Ala Ser Ala Tyr Asn Gly Asn Asp Thr Gln Gly Trp Asn Asp
          20   25   30

Lys -Phe His Xaa Xaa Ser Val Lys Thr Gln Thr Xaa
          35   40

(2) INFORMATION FOR SEQ ID NO: 243:

          (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 51 amino acids
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

Met Ile Ser Asp Ala Gly Ala Gly Phe Gly Val Phe Leu Leu Val Pro
 1   5   10   15

Arg Ala Gly His Cys Trp Gly Ala Gly Lys Pro Leu Pro Ser Cys Pro
          20   25   30

Ser Val Ala Ser Ile Pro Ser Trp Val Leu Pro Ser Phe Leu Glu Arg
          35   40   45

Gly Arg Xaa
          50

(2) INFORMATION FOR SEQ ID NO: 244:

          (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 43 amino acids
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

Met Val Gln Thr Ile Gln Asp Phe Leu Ser Leu Phe Ser Thr Pro Ile
 1   5   10   15

Phe Leu Leu Leu Leu Met Phe Glu Thr Leu Ser Leu Ala Pro Ala Trp
          20   25   30

492

```
Leu Lys Pro Leu Arg Val Thr Ser His Ser Xaa
         35                  40
```

5

(2) INFORMATION FOR SEQ ID NO: 245:

        (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 61 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

```
15  Met Ile Leu Met Pro Gly Leu Gly Thr Ser Arg Gln Arg Ser Val Pro
     1               5              10                15

    Phe Val Pro Thr Leu Asn Ala Ser Thr Pro Gly Ala Met Thr Gly Pro
                 20              25              30
20
    Thr Ala Thr Leu Thr Ser Cys Gln Trp Thr Thr Ala Cys Arg Val Ser
             35              40              45

    Trp Ala Asn Gly Trp Thr Ser Leu Arg Thr Phe Arg Xaa
25       50              55              60
```


(2) INFORMATION FOR SEQ ID NO: 246:
30
        (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 36 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
35   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

```
    Met Ser His His Ala Gln Pro Arg Phe Leu Leu Ile Thr Met Leu Leu
     1               5              10                15

40  Gln Glu Ala Lys Pro Val Ser Asn Ile Pro His Leu Leu Glu Ser Trp
                 20              25              30

    Tyr Phe Gly Xaa
             35
```
45

(2) INFORMATION FOR SEQ ID NO: 247:

50   (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 33 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:
55
```
    Met Asn Ser Leu Phe Trp Met Ile Leu Leu Pro Val Ser Gln Asp Gln
     1               5              10                15

    Val Val Glu Gly Leu Gln Gly Gly Phe Ser Gln Ile His Met Arg Ile
60               20              25              30
```

Leu Arg Lys His Leu Xaa
        35

5

(2) INFORMATION FOR SEQ ID NO: 248:

        (i) SEQUENCE CHARACTERISTICS:
10   (A) LENGTH: 211 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear
        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

15 Met Ser Arg Ser Xaa Asp Val Thr Asn Thr Thr Phe Leu Leu Met Ala
     1   5   10   15

    Ala Ser Ile Tyr Leu His Asp Gln Asn Pro Asp Ala Ala Leu Arg Ala
20   20   25   30

    Leu His Gln Gly Asp Ser Leu Glu Cys Thr Ala Met Thr Val Gln Ile
                 35   40   45

    Leu Leu Lys Leu Asp Arg Leu Asp Leu Ala Arg Lys Glu Leu Lys Arg
25   50   55   60

    Met Gln Asp Leu Asp Glu Asp Ala Thr Leu Thr Gln Leu Ala Thr Ala
     65   70   75   80

30 Trp Val Ser Leu Ala Thr Gly Gly Glu Lys Leu Gln Asp Ala Tyr Tyr
                     85   90   95

    Ile Phe Gln Glu Met Ala Asp Lys Cys Ser Pro Thr Leu Leu Leu Leu
                 100   105   110

35

    Asn Gly Gln Ala Ala Cys His Met Ala Gln Gly Arg Trp Glu Ala Ala
                 115   120   125

    Glu Gly Leu Leu Gln Glu Ala Leu Asp Lys Asp Ser Gly Tyr Pro Glu
40   130   135   140

    Thr Leu Val Asn Leu Ile Val Leu Ser Gln His Leu Gly Lys Pro Pro
    145   150   155   160

45 Glu Val Thr Asn Arg Tyr Leu Ser Gln Leu Lys Asp Ala His Arg Ser
                 165   170   175

    His Pro Phe Ile Lys Glu Tyr Gln Ala Lys Glu Asn Asp Phe Asp Arg
                 180   185   190

50

    Leu Val Leu Gln Tyr Ala Pro Ser Ala Glu Ala Gly Pro Glu Leu Ser
                 195   200   205

    Gly Pro Xaa
55   210

(2) INFORMATION FOR SEQ ID NO: 249:
60

```
            (i)  SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 548 amino acids
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

    Met Glu Asp Ser Glu Ala Leu Gly Phe Glu His Met Gly Leu Asp Pro
     1               5                  10                  15

    Arg Leu Leu Gln Ala Val Thr Asp Leu Gly Trp Ser Arg Pro Thr Leu
                20                  25                  30

    Ile Gln Glu Lys Ala Ile Pro Leu Ala Leu Glu Gly Lys Asp Leu Leu
                35                  40                  45

    Ala Arg Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Tyr Ala Ile Pro
                50                  55                  60

    Met Leu Gln Leu Leu His Arg Lys Ala Thr Gly Pro Val Val Glu
    65                  70                  75                  80

    Gln Ala Val Arg Gly Leu Val Leu Val Pro Thr Lys Glu Leu Ala Arg
                85                  90                  95

    Gln Ala Gln Ser Met Ile Gln Gln Leu Ala Thr Tyr Cys Ala Arg Asp
                100                 105                 110

    Val Arg Val Ala Asn Val Ser Ala Ala Glu Asp Ser Val Ser Gln Arg
                115                 120                 125

    Ala Val Leu Met Glu Lys Pro Asp Val Val Val Gly Thr Pro Ser Arg
                130                 135                 140

    Ile Leu Ser His Leu Gln Gln Asp Ser Leu Lys Leu Arg Asp Ser Leu
    145                 150                 155                 160

    Glu Leu Leu Val Val Asp Glu Ala Asp Leu Leu Phe Ser Phe Gly Phe
                165                 170                 175

    Glu Glu Glu Leu Lys Ser Leu Leu Cys His Leu Pro Arg Ile Tyr Gln
                180                 185                 190

    Ala Phe Leu Met Ser Ala Thr Phe Asn Glu Asp Val Gln Ala Leu Lys
                195                 200                 205

    Glu Leu Ile Leu His Asn Pro Val Thr Leu Lys Leu Gln Glu Ser Gln
                210                 215                 220

    Leu Pro Gly Pro Asp Gln Leu Gln Gln Phe Gln Val Val Cys Glu Thr
    225                 230                 235                 240

    Glu Glu Asp Lys Phe Leu Leu Leu Tyr Ala Leu Leu Lys Leu Ser Leu
                245                 250                 255

    Ile Arg Gly Lys Ser Leu Leu Phe Val Asn Thr Leu Glu Arg Ser Tyr
                260                 265                 270

    Arg Leu Arg Leu Phe Leu Glu Gln Phe Ser Ile Pro Thr Cys Val Leu
                275                 280                 285
```

```
     Asn Gly Glu Leu Pro Leu Arg Ser Arg Cys His Ile Ile Ser Gln Phe
         290             295         300

5    Asn Gln Gly Phe Tyr Asp Cys Val Ile Ala Thr Asp Ala Glu Val Leu
     305             310         315         320

     Gly Ala Pro Val Lys Gly Lys Arg Arg Gly Arg Gly Pro Lys Gly Asp
             325         330             335

10   Lys Ala Ser Asp Pro Glu Ala Gly Val Ala Arg Gly Ile Asp Phe His
             340         345             350

     His Val Ser Ala Val Leu Asn Phe Asp Leu Pro Pro Thr Pro Glu Ala
         355             360         365

15
     Tyr Ile His Arg Ala Gly Arg Thr Ala Arg Ala Asn Asn Pro Gly Ile
         370             375         380

20   Val Leu Thr Phe Val Leu Pro Thr Glu Gln Phe His Leu Gly Lys Ile
     385             390         395             400

     Glu Glu Leu Leu Ser Gly Glu Asn Arg Gly Pro Ile Leu Leu Pro Tyr
             405         410             415

25   Gln Phe Arg Met Glu Glu Ile Glu Gly Phe Arg Tyr Arg Cys Arg Asp
             420         425             430

     Ala Met Arg Ser Val Thr Lys Gln Ala Ile Arg Glu Ala Arg Leu Lys
             435         440         445

30
     Glu Ile Lys Glu Glu Leu Leu His Ser Glu Lys Leu Lys Thr Tyr Phe
         450             455         460

     Glu Asp Asn Pro Arg Asp Leu Gln Leu Leu Arg His Asp Leu Pro Leu
35   465             470         475             480

     His Pro Ala Val Val Lys Pro His Leu Gly His Val Pro Asp Tyr Leu
             485         490             495

40   Val Pro Pro Ala Leu Arg Gly Leu Val Arg Pro His Lys Lys Arg Lys
             500         505         510

     Lys Leu Ser Ser Ser Cys Arg Lys Ala Lys Arg Ala Lys Ser Gln Asn
             515         520         525

45
     Pro Leu Arg Ser Phe Lys His Lys Gly Lys Lys Phe Arg Pro Thr Ala
         530             535         540

     Lys Pro Ser Xaa
50   545
```

```
     (2) INFORMATION FOR SEQ ID NO: 250:

55
             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 299 amino acids
                 (B) TYPE: amino acid
                 (D) TOPOLOGY: linear
60           (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:
```

496

```
     Met Thr Thr Val Pro Pro Ser Pro Arg Pro Met Ser Arg Pro Ser Glu
      1           5           10              15

  5  Arg Asn Met Arg Arg Pro Arg Gly Pro Ser Pro Leu Pro Ala Ser Pro
              20          25              30

     Arg Asn Ser Thr Pro Asp Glu Pro Asp Val His Phe Ser Lys Lys Phe
          35              40              45
 10
     Leu Asn Val Phe Met Ser Gly Arg Ser Arg Ser Ser Ser Ala Glu Ser
          50              55              60

     Phe Gly Leu Phe Ser Cys Ile Ile Asn Gly Glu Glu Gln Glu Gln Thr
 15   65              70              75              80

     His Arg Ala Ile Phe Arg Phe Val Pro Arg His Glu Asp Glu Leu Glu
                  85              90              95

 20  Leu Glu Val Asp Asp Pro Leu Leu Val Glu Leu Gln Ala Glu Asp Tyr
      -           100             105             110

     Trp Tyr Glu Ala Tyr Asn Met Arg Thr Gly Ala Arg Gly Val Phe Pro
              115             120             125
 25
     Ala Tyr Tyr Ala Ile Glu Val Thr Lys Glu Pro Glu His Met Ala Ala
          130             135             140

     Leu Ala Lys Asn Ser Asp Trp Val Asp Gln Phe Arg Val Lys Phe Leu
 30  145             150             155             160

     Gly Ser Val Gln Val Pro Tyr His Lys Gly Asn Asp Val Leu Cys Ala
                  165             170             175

 35  Ala Met Gln Lys Ile Ala Thr Thr Arg Arg Leu Thr Val His Phe Asn
              180             185             190

     Pro Pro Ser Ser Cys Val Leu Glu Ile Ser Val Arg Gly Val Lys Ile
              195             200             205
 40
     Gly Val Lys Ala Asp Asp Ser Gln Glu Ala Lys Gly Asn Lys Cys Ser
          210             215             220

     His Phe Phe Gln Leu Lys Asn Ile Ser Phe Cys Gly Tyr His Pro Lys
 45  225             230             235             240

     Asn Asn Lys Tyr Phe Gly Phe Ile Thr Lys His Pro Ala Asp His Arg
                  245             250             255

 50  Phe Ala Cys His Val Phe Val Ser Glu Asp Ser Thr Lys Ala Leu Ala
                  260             265             270

     Glu Ser Val Gly Arg Ala Phe Gln Gln Phe Tyr Lys Gln Phe Val Glu
              275             280             285
 55
     Tyr Thr Cys Pro Thr Glu Asp Ile Tyr Leu Glu
          290             295
```

60

497

(2) INFORMATION FOR SEQ ID NO: 251:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 40 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

```
Leu Leu Tyr Leu Leu Lys Val Xaa Val Ile Phe Val Phe Ser Ser Ser
 1               5               10              15

Lys Gly Val Thr Leu Val Ser Met Asn Leu Thr Ser Phe Phe Val Ser
            20              25              30

Ser Val Leu Ala Cys Phe Ser Xaa
        35              40
```

(2) INFORMATION FOR SEQ ID NO: 252:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 594 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

```
Met Pro Ala Ser Ser Leu Glu Ser Arg Ser Phe Leu Leu Ala Lys Lys
 1               5               10              15

Ser Gly Glu Asn Val Ala Lys Phe Ile Ile Asn Ser Tyr Pro Lys Tyr
            20              25              30

Phe Gln Lys Asp Ile Ala Glu Pro His Ile Pro Cys Leu Met Pro Glu
        35              40              45

Tyr Phe Glu Pro Gln Ile Lys Asp Ile Ser Glu Ala Ala Leu Lys Glu
        50              55              60

Arg Ile Glu Leu Arg Lys Val Lys Ala Ser Val Asp Met Phe Asp Gln
 65              70              75              80

Leu Leu Gln Ala Gly Thr Thr Val Ser Leu Glu Thr Thr Asn Ser Leu
            85              90              95

Leu Asp Xaa Leu Cys Tyr Tyr Gly Asp Gln Glu Pro Ser Thr Asp Tyr
            100             105             110

His Phe Gln Gln Thr Gly Gln Ser Glu Ala Leu Glu Glu Glu Asn Asp
        115             120             125

Glu Thr Ser Arg Arg Lys Ala Gly His Gln Phe Gly Val Thr Trp Arg
        130             135             140

Ala Lys Asn Asn Ala Glu Arg Ile Phe Ser Leu Met Pro Glu Lys Asn
145             150             155             160

Glu His Ser Tyr Cys Thr Met Ile Arg Gly Met Val Lys His Arg Ala
            165             170             175
```